

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 24, 2003, 11:01:22 ; Search time 29 Seconds
(without alignments)
71.051 Million cell updates/sec

Title: US-09-147-490-1

Perfect score: 58

Sequence: 1 LVVYPWTQRF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	58	100.0	17	4	Q9UM85	Q9um85 homo sapien
2	58	100.0	59	4	Q9BXA2	Q9bxa2 homo sapien
3	58	100.0	61	4	Q14485	Q14485 homo sapien
4	58	100.0	61	4	Q14484	Q14484 homo sapien
5	58	100.0	61	4	Q9UBV6	Q9ubv6 homo sapien
6	58	100.0	89	4	Q9UP81	Q9up81 homo sapien
7	58	100.0	101	4	Q14477	Q14477 homo sapien
8	58	100.0	101	4	Q14476	Q14476 homo sapien
9	58	100.0	105	4	Q9BWU5	Q9bwu5 homo sapien
10	58	100.0	111	4	Q9BWV6	Q9bwv6 homo sapien
11	58	100.0	113	6	O02770	O02770 callithrix
12	58	100.0	115	4	Q9GZL9	Q9gzl9 homo sapien
13	58	100.0	123	4	Q14474	Q14474 homo sapien
14	58	100.0	125	6	Q28221	Q28221 cebus albif
15	58	100.0	125	6	O13072	O13072 callithrix
16	58	100.0	125	6	Q28799	Q28799 pan troglod

17	58	100.0	128	4	Q9UK54	Q9uk54 homo sapien
18	58	100.0	129	4	Q9UNL6	Q9unl6 homo sapien
19	58	100.0	133	6	Q28552	Q28552 ovis aries
20	58	100.0	142	6	Q95233	Q95233 perodicticu
21	58	100.0	142	6	O13071	O13071 callithrix
22	58	100.0	145	6	Q9GJY8	Q9gjy8 callicebus
23	58	100.0	146	6	Q28460	Q28460 mlrounga an
24	58	100.0	147	4	Q9BX96	Q9bx96 homo sapien
25	58	100.0	147	4	Q96FH7	Q96fh7 homo sapien
26	58	100.0	147	4	Q96FH6	Q96fh6 homo sapien
27	58	100.0	147	4	O8WXT7	O8wxt7 homo sapien
28	58	100.0	147	6	Q9GJS7	Q9gjs7 callithrix
29	58	100.0	147	6	Q9GLX7	Q9glx7 salmirel sci
30	58	100.0	147	6	Q9GLX6	Q9glx6 salmirel ust
31	58	100.0	147	6	Q9GLX5	Q9glx5 aotus nancy
32	58	100.0	147	6	Q28779	Q28779 pan paniscu
33	58	100.0	147	6	Q29415	Q29415 cebus oliva
34	58	100.0	147	6	Q03901	Q03901 galago cras
35	58	100.0	147	6	Q03903	Q03903 macaca mula
36	58	100.0	147	11	O88752	O88752 rattus norv
37	58	100.0	152	4	Q14491	Q14491 homo sapien
38	58	100.0	155	4	Q14403	Q14403 homo sapien
39	58	100.0	175	4	Q14473	Q14473 homo sapien
40	57	98.3	15	13	Q90594	Q90594 gallus gall
41	57	98.3	57	4	O95408	O95408 homo sapien
42	57	98.3	61	11	Q99MQ6	Q99mq6 cricetulus
43	57	98.3	73	11	O64372	O64372 peromyscus
44	57	98.3	75	11	Q99MQ7	Q99mq7 cricetulus
45	57	98.3	125	11	Q9CZG2	Q9czg2 mus musculu

ALIGNMENTS

RESULT 1

Q9UM85 PRELIMINARY; PRT; 17 AA.
ID Q9UM85
AC Q9UM85;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Beta-globin protein (Fragment).
GN BETA-GLOBIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96352914; PubMed=8718696;
RA Rahbar S., Nozari G., Forrest G., Gelbart T., Forman S.J., Beutler E.;
RT "A novel intrachromosomal rearrangement in the beta-globin gene found
in an African-American family.";
RL Hemoglobin 19:375-388(1995).
DR EMBL: S82767; AAD14420.1; -;
DR HSSP: P02023; 1ABW
FT NON_TER 1
SQ SEQUENCE 17 AA; 2104 MW; 41977E5BE5260504 CRC64;

Query Match 100.0%; Score 58; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 2 LVVYPWTQRF 11

RESULT 2

Q9BXA2 PRELIMINARY; PRT; 59 AA.
ID Q9BXA2
AC Q9BXA2;
DT 01-JUN-2001 (Tremblrel. 17, Created)

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DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Beta-globin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kutlar F., Aquinaga P.M., Glendenning M., Kutlar A.;
RT "IVS-I-5 G to C Homozygous Beta Thalassaemia Mutation was Detected in a
RT Kurdish Patient.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; AF348448; AA030154.1; -.
DR HSSP; P02023; 1DXT.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport.
FT NON_TER 59
SQ SEQUENCE 59 AA; 6463 MW; 128EF2C12A13A9D3 CRC64;

Query Match 100.0%; Score 58; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
DB |||||
33 LVVYPWTQRF 42

RESULT 3
Q14485 PRELIMINARY; PRT; 61 AA.
AC Q14485;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Delta-hemoglobin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu J.Z., Harano T., Lanclos K.D., Huisman T.H.;
RT "The beta-delta crossover leading to the beta delta hybrid gene of
RT hemoglobin P-Nilotic is located within 54 base-pairs of the 5' end of
RT exon 2 or between codons 31 and 50.";
RL Biochim. Biophys. Acta 909:208-212(1987).
CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; M25661; AAA53154.1; -.
DR HSSP; P02023; 1DXT.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport.
FT NON_TER 61
SQ SEQUENCE 61 AA; 6661 MW; D5DC4F2CC2DDF822 CRC64;

Query Match 100.0%; Score 58; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.0081;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
DB |||||
33 LVVYPWTQRF 42

Query Match 100.0%; Score 58; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.0081;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
DB |||||
33 LVVYPWTQRF 42

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RESULT 4
Q14484 PRELIMINARY; PRT; 61 AA.
AC Q14484;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Beta-hemoglobin (Fragment).
GN HBB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87299720; PubMed=3620470;
RA Liu J.Z., Harano T., Lanclos K.D., Huisman T.H.;
RT "The beta-delta crossover leading to the beta delta hybrid gene of
RT hemoglobin P-Nilotic is located within 54 base-pairs of the 5' end of
RT exon 2 or between codons 31 and 50.";
RL Biochim. Biophys. Acta 909:208-212(1987).
RN [2]
RP SEQUENCE FROM N.A.
RA Fullerton S.M., Bond J., Schneider J.A., Hamilton B., Harding R.M.,
RA Boyce A.J., Clegg J.B.;
RT "Polymorphism and divergence in the beta-globin replication origin
RT initiation region.";
RL Mol. Biol. Evol. 0:0-0(1999).
CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; M25660; AAA53153.1; -.
DR EMBL; AF186620; AAF08272.1; -.
DR EMBL; AF186606; AAF08258.1; -.
DR EMBL; AF186608; AAF08260.1; -.
DR EMBL; AF186609; AAF08261.1; -.
DR EMBL; AF186610; AAF08262.1; -.
DR EMBL; AF186611; AAF08263.1; -.
DR EMBL; AF186612; AAF08264.1; -.
DR EMBL; AF186613; AAF08265.1; -.
DR EMBL; AF186615; AAF08267.1; -.
DR EMBL; AF186616; AAF08268.1; -.
DR EMBL; AF186617; AAF08269.1; -.
DR EMBL; AF186618; AAF08270.1; -.
DR EMBL; AF186619; AAF08271.1; -.
DR HSSP; P02023; 1DXT.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport.
FT NON_TER 61
SQ SEQUENCE 61 AA; 6691 MW; 905E928EF2C12A13 CRC64;

Query Match 100.0%; Score 58; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.0081;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
DB |||||
33 LVVYPWTQRF 42

RESULT 5
Q9UBV6 PRELIMINARY; PRT; 61 AA.
AC Q9UBV6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Beta-globin (Fragment).
GN HBB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

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RN [1]
RA Fullerton S.M., Bond J., Schneider J.A., Hamilton B., Harding R.M.,
RA Boyce A.J., Clegg J.B.;
RT "Polymorphism and divergence in the beta-globin replication origin
RT initiation region.";
RL Mol. Biol. Evol. 0:0-0(1999).
CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; AF186614; AAF08266.1; -.
DR EMBL; AF186607; AAF08259.1; -.
DR HSP; P02023; IHSB
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport.
FT NON_TER 61
SQ SEQUENCE 61 AA; 6661 MW; 304D818EF2C13435 CRC64;

Query Match 100.0%; Score 58; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.0081;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 33 LVVYPWTQRF 42

RESULT 6
ID Q9UP81 PRELIMINARY; PRT; 89 AA.
AC Q9UP81;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Mutant beta-globin.
GN HBB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA MEDLINE-99250504; PubMed-10233364;
RX Cabeda J.M., Correia C., Estevinho A., Cardoso C., Amorim M.L.,
RA Cleto E., Vale L., Coimbra E., Pinho L., Justica B.;
RT "Unexpected pattern of beta-globin mutations in beta-thalassaemia
RT patients from northern Portugal.";
RL Br. J. Haematol. 105:68-74(1999).
CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; AF059180; AAD30656.1; -.
DR HSP; P02070; IFSX.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport.
SQ SEQUENCE 89 AA; 9689 MW; 4A138B28BEEF0D1 CRC64;

Query Match 100.0%; Score 58; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 33 LVVYPWTQRF 42

RESULT 7
Q14477 PRELIMINARY; PRT; 101 AA.
ID Q14477

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AC Q14477;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE HBB protein (Fragment).
GN HBB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA MEDLINE-84178511; PubMed-6324786;
RX Kimura A., Ohta Y., Fukumaki Y., Takagi Y.;
RT "A fusion gene in man: DNA sequence analysis of the abnormal globin
RT gene of hemoglobin Miyada.";
RL Biochem. Biophys. Res. Commun. 119:968-974(1984).
CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; K01899; AAA52635.1; -.
DR HSP; P02023; IDXT.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR InterPro; IPR002335; Myoglobin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; MYOGLOBIN.
DR Erythrocyte; Heme; Oxygen transport.
FT NON_TER 101
SQ SEQUENCE 101 AA; 10928 MW; F54BFDB224B5DB0F CRC64;

Query Match 100.0%; Score 58; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 33 LVVYPWTQRF 42

RESULT 8
Q14476 PRELIMINARY; PRT; 101 AA.
ID Q14476
AC Q14476;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE G-gamma-hemoglobin gene from Greek HPFH mutant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA MEDLINE-86017015; PubMed-2413469;
RX Gellinas R., Yagi M., Endlich B., Lotshaw H.H.Jr. .,
RA Stamatovannopoulos G.;
RT "Sequences of G-gamma, A-gamma, and beta genes of the Greek (A-gamma)
RT HPFH mutant: evidence for a distal CCAAT box mutation in the A-gamma
RT gene.";
RL Prog. Clin. Biol. Res. 191:125-139(1985).
CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; M3723; AAA35955.1; -.
DR HSP; P02096; IFDH.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; Myoglobin.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; MYOGLOBIN.
DR Erythrocyte; Heme; Oxygen transport.
FT NON_TER 101

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SQ SEQUENCE 101 AA; 11039 MW; 8489D25BBDE29BA5 CRC64;
Query Match 100.0%; Score 58; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
DB 33 LVVYPWTQRF 42

RESULT 9
Q9BWU5
ID Q9BWU5 PRELIMINARY; PRT; 105 AA.
AC Q9BWU5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Mutant hemoglobin beta chain (Fragment).
GN HBB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Kutlar F., Leithner C., Briscoe J., Kutlar A.;
RT "Hemoglobin S (Glu 6 Val) +D-Ibadan (Thr 87 Lys); two beta chain variants were detected in an African-American individual by sequencing of the beta globin gene."
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RL -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
CC DR EMBL; AY027800; AAK15811.1; -.
DR HSSP; P02023; 2HBS.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport.
FT VARIANT 7 88 7
FT NON_TER 105 105 V -> E.
FT SEQUENCE 105 AA; 11501 MW; 8143C84D90C01687 CRC64;

Query Match 100.0%; Score 58; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
DB 33 LVVYPWTQRF 42

RESULT 10
Q9BWV6
ID Q9BWV6 PRELIMINARY; PRT; 111 AA.
AC Q9BWV6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Mutant beta globin.
GN HBB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Kutlar F., Adekunle A.D., Leithner C., Kutlar A.;
RT "Double heterozygous beta thalassemia mutation (Promoter region - 28 A

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RT to C; IVS-II-1 region G to A) was found in a Kuwaiti patient."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; AY027509; AAK20080.1; -.
DR HSSP; P02023; 1DXT.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport.
FT VARIANT 106 106 M -> V.
FT SEQUENCE 111 AA; 12234 MW; 8992F924B5B3903A CRC64;

Query Match 100.0%; Score 58; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
DB 33 LVVYPWTQRF 42

RESULT 11
O02770
ID O02770 PRELIMINARY; PRT; 113 AA.
AC O02770;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Epsilon-globin (Fragment).
OS Callithrix argentata (Black-tailed marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9482;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98121278; PubMed=9461380;
RA Porter C.A., Czelusniak J., Schneider H., Schneider M.P., Sampaio I.,
RA Goodman M.;
RT "Sequences of the primate epsilon-globin gene: implications for RT systematics of the marmosets and other New World primates."
RL Gene 205:59-71(1997).
CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; U97025; AAC39571.1; -.
DR HSSP; P02100; 1A9W.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR InterPro; IPR002335; Myoglobin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; MYOGLOBIN.
DR PROSITE; PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport.
FT NON_TER 113 113
FT SEQUENCE 113 AA; 12499 MW; 994B77D3BEC81D9D CRC64;

Query Match 100.0%; Score 58; DB 6; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
DB 33 LVVYPWTQRF 42

RESULT 12
Q9GZL9
ID Q9GZL9 PRELIMINARY; PRT; 115 AA.
AC Q9GZL9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

```

```

DE Beta-globin (Mutant beta-globin) (Fragment).
GN HBB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang Z., Chu J., Ban G., Shi L., Huang X., Lin K., Tao Y.;
RT "Molecular characterization of beta thalassemia in Yunnan, China.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; AY013302; AAG46185.1; -.
DR EMBL; AY013301; AAG46184.1; -.
DR HSSP; P02023; 1DXT.
DR InterPro; IPR002337; Beta.haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport.
FT NON_TER 115
SQ SEQUENCE 115 AA; 13528 MW; FA179881D9CA8E1B CRC64;

Query Match 100.0%; Score 58; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
   |||||
Db 33 LVVYPWTQRF 42

RESULT 13
Q14474 PRELIMINARY; PRT; 123 AA.
AC Q14474;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE A-gamma-hemoglobin gene from Greek HPFH mutant (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gelinas R., Yagi M., Endlich B., Lotshaw C., Kazazian H.H.Jr. .;
RT "Sequences of G-gamma, A-gamma, and beta genes of the Greek (A-gamma) HPFH mutant: evidence for a distal CCAAT box mutation in the A-gamma gene.";
RL Prog. Clin. Biol. Res. 191:125-139(1985).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; M32724; AAA35953.1; -.
DR HSSP; P02096; 1FDH.
DR InterPro; IPR002337; Beta.haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; MYOGLOBIN.
DR PROSITE; PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport.
FT NON_TER 123
SQ SEQUENCE 123 AA; 13510 MW; 7C427399B2FA2FC1 CRC64;

Query Match 100.0%; Score 58; DB 4; Length 123;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
   |||||
Db 33 LVVYPWTQRF 42

RESULT 14
Q28221 PRELIMINARY; PRT; 125 AA.
AC Q28221;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Gamma-1 globin.
GN GAMMAL1-GLOBIN.
OS Cebus albifrons (White-fronted capuchin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus.
OX NCBI_TaxID=9514;
RN [1]
RP SEQUENCE FROM N.A.
RA Hayasaka K., Skinner C.G., Goodman M., Slightom J.L.;
RT "The gamma-globin genes and their flanking sequences in primates: findings with nucleotide sequences of capuchin monkey and tarsier.";
RL Genomics 18:20-28(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=941102757; PubMed=8276414;
RA Hayasaka K., Skinner C.G., Goodman M., Slightom J.L.;
RT "Reexamination of the African hominoid trichotomy with additional sequences from the primate beta-globin gene cluster.";
RL Mol. Phylogenet. Evol. 1:97-135(1992).
RN [3]
RP SEQUENCE FROM N.A.
RA Hayasaka K., Skinner C.G., Slightom J.L., Goodman M.;
RT "Molecular phylogeny of three platyrrhine primates, capuchin monkey, RT spider monkey, and owl monkey, as inferred from nucleotide sequences of the pseudo-eta-globin gene.";
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; M61409; AAA19703.1; -.
DR HSSP; P02096; 1FDH.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport.
SQ SEQUENCE 125 AA; 13534 MW; AD1C8A32D49179BF CRC64;

Query Match 100.0%; Score 58; DB 6; Length 125;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
   |||||
Db 33 LVVYPWTQRF 42

RESULT 15
Q13072 PRELIMINARY; PRT; 125 AA.
AC Q13072;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Epsilon-globin (Fragment).
OS Callithrix jacchus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=57377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98121278; PubMed=9461380;
RA Porter C.A., Czelusniak J., Schneider H., Schneider M.P., Sampaio I.,

```

```

RA Goodman M.;
RT "Sequences of the primate epsilon-globin gene: implications for
RL systematics of the marmosets and other New World primates.";
RL Gene 205:59-71(1997).
CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; U97024; AAC39570.1; -.
DR HSSP; P02100; 1A9W.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR InterPro; IPR002335; Myogloblin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PRINTS; PR00613; MYOGLOBIN.
DR PROSITE; PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport.
FT NON_TER 125
SQ SEQUENCE 125 AA; 13842 MW; D31A007C586B6C7C CRC64;

Query Match 100.0%; Score 58; DB 6; Length 125;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
DB 33 LVVYPWTQRF 42

```

Search completed: February 24, 2003, 11:03:53
Job time : 31 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 24, 2003, 11:01:21 ; Search time 35 Seconds
(without alignments)
38.072 Million cell updates/sec

Title: US-09-147-490-1
Perfect score: 58
Sequence: 1 LVVYPWTFQF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_101002.*

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16:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT.*
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20:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.*
21:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
22:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	58	100.0	10	17	AAR97348	Peptide fragment c
2	58	100.0	10	18	AAW30318	Peptide haemorphin
3	58	100.0	10	19	AAW37247	Angiotensin IV act
4	58	100.0	10	22	AAU79893	Anti-stress agent
5	58	100.0	74	66	AAU50291	Sequence encoded b
6	58	100.0	74	16	AAR59602	Human beta-globin
7	58	100.0	86	22	AAO07245	Human polypeptide
8	58	100.0	104	22	AAU30074	Novel human secret
9	58	100.0	110	22	AAO02538	Human polypeptide
10	58	100.0	112	16	AAR89262	Human beta-globin

ALIGNMENTS

RESULT 1	
AAR97348	
ID	AAR97348 standard; Protein; 10 AA.
XX	
XX	AAR97348;
XX	
DT	17-OCT-1996 (first entry)
XX	
DE	Peptide fragment of haemoglobin B (Haemorphin 10).
XX	
KW	haemoglobin; INPROL; stem cell proliferation; B lymphocytes;
KW	B cells; chemotherapy; cancer; haematopoietic cells; marrow; blood;
KW	myeloproliferative disease; autoimmune disease; adjuvant;
KW	vaccination; immunodepression; gene therapy.

11	58	100.0	112	16	AA889261	Human beta-globin
12	58	100.0	121	21	AAG61752	Human secreted pro
13	58	100.0	124	21	AAU29598	Novel human secret
14	58	100.0	127	22	AA013066	Human polypeptide
15	58	100.0	128	22	AA009585	Human polypeptide
16	58	100.0	137	22	AAU30769	Novel human secret
17	58	100.0	140	22	AAU79250	Human protein SEQ
18	58	100.0	141	18	AAW30718	Haemoglobin beta(-
19	58	100.0	142	22	AAU29784	Novel human secret
20	58	100.0	143	22	AAU29796	Novel human secret
21	58	100.0	143	22	AAU29798	Novel human secret
22	58	100.0	143	22	AAU29847	Novel human secret
23	58	100.0	143	22	AAU29890	Novel human secret
24	58	100.0	143	22	AAU29920	Novel human secret
25	58	100.0	143	22	AAU29929	Novel human secret
26	58	100.0	143	22	AAU29955	Novel human secret
27	58	100.0	143	22	AAU29961	Novel human secret
28	58	100.0	143	22	AAU29977	Novel human secret
29	58	100.0	143	22	AAU30020	Novel human secret
30	58	100.0	143	22	AAU30022	Novel human secret
31	58	100.0	143	22	AAU30024	Novel human secret
32	58	100.0	143	22	AAU30028	Novel human secret
33	58	100.0	143	22	AAU30030	Novel human secret
34	58	100.0	143	22	AAU30083	Novel human secret
35	58	100.0	143	22	AAU30099	Novel human secret
36	58	100.0	143	22	AAU30132	Novel human secret
37	58	100.0	143	22	AAU32926	Novel human secret
38	58	100.0	144	13	AA829611	Mutant human beta-
39	58	100.0	144	14	AA839726	HbA McKees Rock
40	58	100.0	144	19	AA873382	Human haemoglobin
41	58	100.0	145	13	AA820303	Val(1) to Met, His
42	58	100.0	145	13	AA820305	Val(1) to Met, His
43	58	100.0	145	13	AA820306	Met(1), His(2) del
44	58	100.0	145	22	AAU10346	Human polypeptide
45	58	100.0	146	9	AA81301	Mutant beta-globin

PT - useful in mammals, e.g. for protecting stem cells from antiviral
PT agents, treating cancer, and maintaining mammalian haematopoietic
PT stem cells *ex vivo*
PS
PS Claim 17: Page 65; 101pp; English.
XX
XX Compositions (INPROL) comprising a polypeptide selected from the
CC haemoglobin alpha, beta, gamma, delta, epsilon or zeta chains and a
CC carrier may be used to inhibit stem cell proliferation. INPROL can
CC also be used for stimulating the growth of B cells and can be used
CC with radio-or chemotherapy to treat cancer in mammals by
CC differentially protecting normal stem cells and not cancer cells
CC from such therapy. INPROL is also useful for maintaining mammalian
CC haematopoietic stem cells *ex vivo* (particularly bone marrow,
CC peripheral blood or cord blood cells); for the *ex vivo* expansion of
CC haematopoietic cells when used in combination with a stimulatory
CC cytokine. INPROL can also be used to treat myeloproliferative or
CC autoimmune disease. INPROL is also useful as an adjuvant in the
CC vaccination of mammals and can be used to treat a mammal with
CC immunodepression caused by stem cell proliferation. INPROL can also
CC be used in gene therapy. This peptide fragment of human haemoglobin
CC B corresponds to amino acids 32-41 of the mature protein given in
CC AAR97358.
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 58; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LVVYPWTQRF 10
Db 1 LVVYPWTQRF 10
|||||
RESULT 2
AAW30318
ID AAW30318 standard; peptide: 10 AA.
XX
XX AAW30318;
AC
XX
XX 20-APR-1998 (first entry)
DT
XX
XX Peptide haemorphin 10 with opiate activity.
DE
XX
XX INPROL; stem cell; inhibition; stimulation; proliferation; myoglobin;
KW alpha chain; haemoglobin; radiotherapy; chemotherapy; cancer;
KW differential protection; stem cell hypoproliferation; aplastic anaemia;
KW stem cell exhaustion; haemorphin; opiate activity.
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX WO9736922-A1.
PN
XX
XX 09-OCT-1997.
PD
XX
XX 03-APR-1997; 97WO-US05601.
PF
XX
XX 03-APR-1996; 96US-0627173.
PR
XX
XX (PRON-) PRO-NEURON INC.
FA
XX
XX Tsyrova I, Wolpe SD;
PI
XX
XX WPI; 1997-503044/46.
DR
XX
XX Haemoglobin alpha chain derivatives - used to inhibit or stimulate
PT stem cell proliferation, for treatment of cancer, immune depression
PT etc
PT
XX
XX Claim 49; Page 117; 162pp; English.
PS
XX

CC The present peptide is derived from amino acids 32-41 of the beta
CC chain of adult human haemoglobin. The peptide has sequence similarity
CC and biological activity similar to other atypical opiate peptides. The
CC peptide can stimulate or inhibit stem cell proliferation, similar to
CC INPROL compounds. The peptide is used to inhibit stem cell proliferation,
CC particularly during radiotherapy or chemotherapy of cancer, but more
CC generally wherever a mammal is exposed to an agent, e.g. an antiviral,
CC that damages or destroys stem cells. It can also be used for differential
CC protection of normal stem cells, but not cancer cells, from chemotherapy
CC or radiation, particularly after normal stem cells have been induced to
CC proliferate by therapeutic treatment. The peptide can also be used for
CC control of stem cell hypoproliferation (e.g. aplastic anaemia), for
CC treating or preventing stem cell exhaustion (e.g. where caused by
CC acquired immune deficiency syndrome), and to treat or prevent
CC immunodeficiency. INPROL can also be used for treating pain in a mammal.
CC INPROL and related compounds reversibly inhibit or stimulate stem cells
CC depending on the dose, so allow precise control over cycling of these
CC cells.
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 58; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LVVYPWTQRF 10
Db 1 LVVYPWTQRF 10
|||||
RESULT 3
AAW37247
ID AAW37247 standard; peptide: 10 AA.
XX
XX AAW37247;
AC
XX
XX 18-JUN-1998 (first entry)
DT
XX
XX Angiotensin IV activity exhibiting neuroactive peptide LVV-haemorphin-7.
DE
XX
XX Angiotensin IV; neuroactive; Alzheimer's disease; modulator; dementia;
KW neuronal development; vasoeffective; neuropathy; brain injury;
KW LVV-haemorphin-7.
XX
XX Synthetic.
OS
XX Macaca fascicularis.
XX
XX WO9801465-A1.
PN
XX
XX 15-JAN-1998.
PD
XX
XX 09-JUL-1997; 97WO-AU00436.
PF
XX
XX 09-JUL-1996; 96AU-0000893.
PR
XX
XX (FLOR-) FLOREY INST EXPERIMENTAL PHYSIOLOGY.
PA
XX
XX Aldred PG, Chai SY, Lew RA, Mendelsohn FAO, Moeller I;
PI Smith IA;
XX
XX WPI; 1998-100995/09.
DR
XX
XX Neuro-active peptide with activities of angiotensin IV and related
PT DNA - antagonists and oligo:nucleotide(s), useful for modulating
PT neuronal development and activity of motor and cholinergic neurons
PT
XX
XX Claim 1; Page 45; 65pp; English.
PS
XX
XX This LVV-haemorphin-7 is a neuroactive peptide with at least 1 of the
CC activities of angiotensin IV. This is an agonist of the angiotensin IV
CC receptor and is its endogenous ligand in the brain. It can modulate
CC learning or behaviour and has vasoactive effects and can dilate cerebral
CC arteries, increase renal blood flow and stereotypy behaviour, facilitate
CC

CC memory retrieval, induce neurite remodelling, and alleviate effects of
 CC spinal cord injuries. This peptide and its antagonists are used to
 CC modulate activity of motor, cholinergic neurons and neuronal development.
 CC Specific applications are in treatment of dementia, Alzheimer's disease,
 CC neurodegeneration (involving cholinergic, motor or sensory pathways),
 CC sensory and motor peripheral neuropathy, brain injury and spinal cord
 CC injury (caused by one or more of trauma, hypoxia and/or vascular
 CC disease). Antibodies specific for the peptide can be used to determine
 CC its amount of in tissues and tissue regions.
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 58; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00065;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 |
 Db 1 LVVYPWTQRF 10

RESULT 4

ID AAU79893 standard; Peptide; 10 AA.

XX AC AAU79893;

DT 15-JUL-2002 (first entry)

DE Anti-stress agent and anti-stress food associated peptide #5.

KW Anti-stress agent; anti-stress food; anxiolytic; tranquilliser;
 KW stress.

XX Synthetic.

XX JP2001226281-A.

XX 21-AUG-2001.

PF 10-FEB-2000; 2000JP-0033569.

XX 10-FEB-2000; 2000JP-0033569.

XX (ITOH-) ITO HAM KK.

XX WPI: 2001-609888/70.

PT An anti-stress agent and an anti-stress food -

XX Disclosure; Page 2; 7pp; Japanese.

CC The invention describes an anti-stress agent containing a peptide
 CC and/or its pharmacologically allowable salt as the active component.
 CC The anti-stress agent and the anti-stress food function as anxiolytics
 CC and tranquillisers and can be used for decreasing and preventing mental
 CC and physical symptoms caused by various stresses. This sequence
 CC represents a peptide included in the anti-stress agent and the
 CC anti-stress food of the invention.

XX Sequence 10 AA;

Query Match 100.0%; Score 58; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00065;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 |
 Db 1 LVVYPWTQRF 10

RESULT 5

AAP50291

ID AAP50291 standard; Protein; 74 AA.
 XX
 AC AAP50291;
 XX
 DT 30-NOV-1991 (first entry)
 XX
 DE Sequence encoded by second exon of rabies glycoprotein gene.
 XX
 KW Rabies vaccine; therapy; glycoprotein; antigen; diagnosis.
 XX
 OS Rabies virus.
 XX
 PN W08501516-A.
 XX
 PD 11-APR-1985.
 XX
 PF 02-OCT-1984; 84WO-4000217.
 XX
 PR 27-MAR-1984; 84FR-0004754.
 PR 03-OCT-1984; 84FR-0015716.
 PR 03-OCT-1983; 83FR-0015716.
 XX
 PA (TRAN-) TRANSGENE SA.
 PA (LATH/) LATHE R.

XX Lathe R, Kieny MP, Lemoine Y, Loison G, Aigle M;

XX WPI: 1985-098845/16.

XX N-PSDB; AAN50333.

XX Vector for expressing rabies antigen - in eucaryotic cells,
 PT useful for making vaccines and curative agents

XX Example; Fig 10; 62pp; French.

XX The inventors claim a vector for expressing a rabies antigen protein
 CC in eucaryotic cells. After glycosylation with a yeast (specifically
 CC at ASP residues 204 and 319), the recombinant antigen protein is
 CC useful as a vaccine or curative agent. The coding sequence in the
 CC vector can be followed by an intron (see AAN50333.N50334) or sites of
 CC polyadenylation.
 XX
 SQ Sequence 74 AA;

Query Match 100.0%; Score 58; DB 6; Length 74;
 Best Local Similarity 100.0%; Pred. No. 0.0055;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
 |
 Db 2 LVVYPWTQRF 11

RESULT 6

AAR69602

ID AAR69602 standard; Protein; 74 AA.

XX AC AAR69602;

XX 25-SEP-1995 (first entry)

DT Human beta-globin encoded by optimised exon 2.

DE Beta-globin; optimised codons; exon 2.

XX Synthetic.

XX W09504744-A.

XX 16-FEB-1995.

XX 29-JUL-1994; 94WC-US08630.

XX

PR 11-AUG-1993; 93US-0105989.
 XX (DNXD-) DNX CORP.
 XX Khoury-christianson AM, Kumar R, Midha S., Paulhiac C;
 PI Sharma A;
 XX WPI; 1995-090838/12.
 DR N-PSDB; AAQ83723.
 XX
 XX Production of human haemoglobin in transgenic pigs - by
 PT introducing gene constructs comprising human alpha and beta
 PT globin genes into pig ova, for an efficient source of haemoglobin
 PT for use in e.g. transfusions
 XX
 XX Example; Fig 39; 155pp; English.
 PS
 XX Human alpha-globin is expressed in transgenic pigs at higher levels
 CC than human beta-globin. One approach to increasing the level of
 CC expressed beta-globin is to engineer the human beta-globin gene
 CC from the promoter region through the coding sequence and into the
 CC polyA site and 3' UTR to be similar to pig beta-globin gene, but
 CC without altering the AA sequence from that of authentic wt human
 CC beta-globin. PCR was used to optimise human beta-globin gene for
 CC porcine expression. Equivalent fragments of the human and pig beta-
 CC globin coding sequences in exons 1, 2 and 3 are depicted in
 CC AAQ83716/Q83719, AAQ83717/Q83720 and AAQ83718/Q83721, respectively.
 CC These pairs of sequences may be compared for differences. Optimised
 CC human beta-globin coding sequences for exons 1, 2 and 3 are depicted in
 CC AAQ83722, AAQ83723 and AAQ83724, respectively. These sequences may be
 CC compared with AAQ83716, AAQ83717 and AAQ83718 respectively. The AA
 CC sequences encoded by the optimised human beta-globin coding sequences
 CC are given in AAR69601, AAR69602, AAR69603.
 XX
 XX Sequence 74 AA;
 SQ
 Query Match 100.0%; Score 58; DB 16; Length 74;
 Best Local Similarity 100.0%; Pred. No. 0.0055;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPWTQRF 10
 Db ||||||
 2 LVVYPWTQRF 11
 RESULT 7
 ID AAQ07245 standard; Protein: 86 AA.
 XX
 AC AAQ07245;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 21137.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200164835-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US04927.
 XX
 XX 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 PR
 XX (HYSE-) HYSEQ INC.
 PA
 XX

PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-514838/56.
 DR N-PSDB; AAI87176.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 XX
 PS Claim 20; SEQ ID NO 21137; 1399pp + Sequence Listing; English.
 XX
 CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 86 AA;
 Query Match 100.0%; Score 58; DB 22; Length 86;
 Best Local Similarity 100.0%; Pred. No. 0.0065;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPWTQRF 10
 Db ||||||
 39 LVVYPWTQRF 48
 RESULT 8
 ID AAU30074 standard; Protein: 104 AA.
 XX
 AC AAU30074;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #565.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-611725/70.
 XX
 CC Nucleic acids encoding a range of human polypeptides, useful in genetic
 CC vaccination, testing and therapy -
 XX
 PS Claim 20; Page 234; 765pp; English.
 XX

CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.

XX
 SQ Sequence 104 AA;

Query Match 100.0%; Score 58; DB 22; Length 104;
 Best Local Similarity 100.0%; Pred. No. 0.0079;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||
 Db 33 LVVYPWTQRF 42

RESULT 9

AA002538

ID AA002538 standard; Protein; 110 AA.
 AC
 AC AA002538;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 16430.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

XX WO200164835-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US04927.

XX 28-FEB-2000; 2000US-0515126.

PR 18-MAY-2000; 2000US-0577409.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514838/56.

DR N-PSDB; AA182469.

XX Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -

XX Claim 20; SEQ ID NO 16430; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AA000010-AA013910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or

CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.

CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 110 AA;

Query Match 100.0%; Score 58; DB 22; Length 110;

Best Local Similarity 100.0%; Pred. No. 0.0084;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||
 Db 17 LVVYPWTQRF 26

RESULT 10

AA89262

ID AAR89262 standard; peptide; 112 AA.

XX

AC AAR89262;

XX 04-MAR-1996 (first entry)

XX Human beta-globin mutant Val90, Met91, Ser93, Glu94.

DE Human beta-globin; mutant Val90, Met91, Ser93, Glu94; hypoxic cells;
 KW increased oxygenation; radiation therapy; vascular diseases.

XX Homo sapiens.

XX US5428007-A.

XX 27-JUN-1995.

XX 06-OCT-1989; 89US-0417949.

XX 06-OCT-1989; 89US-0417949.

PR 09-OCT-1992; 92US-0959286.

PR 28-APR-1994; 94US-0235118.

XX (UYA) UNIV YALE.

XX Baserga SJ, Fischer JJ;

XX WPI; 1995-240064/31.

XX Increasing tissue oxygen in hypoxic cells - by administering a pure
 PT mutant alpha or beta haemoglobin having a low oxygen affinity.

XX Example 3; Columns 3-6; 10pp; English.

XX AAR89262 is the human beta-globin mutant Val90, Met91, Ser93, Glu94.
 CC The mutant globin can be used to increase tissue oxygenation in
 CC hypoxic cells, to increase oxygenation in tumours to enhance the
 CC effects of radiation therapy or as a blood replacement or
 CC treatment in vascular diseases.

XX Sequence 112 AA;

Query Match 100.0%; Score 58; DB 16; Length 112;

Best Local Similarity 100.0%; Pred. No. 0.0086;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||
 Db 32 LVVYPWTQRF 41

RESULT 11

AA89261
ID AAR89261 standard; peptide; 112 AA.

XX AC AAR89261;
XX DT 04-MAR-1996 (first entry)

XX DE Human beta-globin mutant Gln/Lys90 and Asp108.
XX KW Human beta-globin; mutant Gln/Lys90 and Asp108; hypoxic cells;
XX KW increased oxygenation; radiation therapy; vascular diseases.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT Misc-difference 90
XX FT /label= Gln, Lys

XX PN US5428007-A.
XX PD 27-JUN-1995.

XX PF 06-OCT-1989; 89US-0417949.
XX PR 06-OCT-1989; 89US-0417949.
XX PR 09-OCT-1992; 92US-0959286.
XX PR 28-APR-1994; 94US-0235118.

XX PA (UYUA) UNIV YALE.

XX PI Baserga SJ, Fischer JJ;

XX DR WPI; 1995-240064/31.

XX PT Increasing tissue oxygen in hypoxic cells - by administering a pure
XX PT mutant alpha or beta haemoglobin having a low oxygen affinity.
XX PS Example 3; Columns 5-6; 10pp; English.

XX CC AAR89261 is the human beta-globin mutant Gln/Lys90 and Asp108.
XX CC The mutant globin can be used to increase tissue oxygenation in
XX CC hypoxic cells, to increase oxygenation in tumours to enhance the
XX CC effects of radiation therapy or as a blood replacement or
XX CC treatment in vascular diseases.

XX SQ Sequence 112 AA;

Query Match 100.0%; Score 58; DB 16; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTQRF 10
| | | | | | | |
Db 32 LVVYPWTQRF 41

RESULT 12

AG01752
ID AAG01752 standard; Protein; 121 AA.

XX AC AAG01752;

XX DT 06-OCT-2000 (first entry)

XX DE Human secreted protein, SEQ ID NO: 5833.

XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX KW gene therapy; chromosome mapping.

XX OS Homo sapiens.

XX

PN EPI033401-A2.

XX PD 06-SEP-2000.

XX PF 21-FEB-2000; 2000EP-0200610.

XX PR 26-FEB-1999; 99US-0122487.

XX PA (GEST) GENSET.

XX PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX DR WPI; 2000-500381/45.

XX DR N-PSDB; AAC01758.

XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX PS Claim 13; SEQ ID 5833; 71pp + CD-ROM; English.

XX CC The present sequence is a polypeptide encoded by one of a large number
XX CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
XX CC were prepared from total human RNAs or polyA+ RNAs derived from 30
XX CC different tissues. EST sequences usually correspond mainly to the 3'
XX CC untranslated region (UTR) of the mRNA because they are often obtained
XX CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
XX CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
XX CC those cases where longer cDNA sequences have been obtained, the full 5'
XX CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
XX CC ends and can therefore be used to obtain full length cDNAs and genomic
XX CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
XX CC chromosome mapping procedures. They are used to obtain upstream
XX CC regulatory sequences and to design expression and secretion vectors.

XX SQ Sequence 121 AA;

Query Match 100.0%; Score 58; DB 21; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTQRF 10
| | | | | | | |
Db 33 LVVYPWTQRF 42

RESULT 13

AAU29698
ID AAU29698 standard; Protein; 124 AA.

XX AC AAU29698;

XX DT 18-DEC-2001 (first entry)

XX DE Novel human secreted protein #189.

XX KW Human; vaccination; gene therapy; nutritional supplement;
XX KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX OS Homo sapiens.

XX PN WO200179449-A2.

XX PD 25-OCT-2001.

XX PF 16-APR-2001; 2001WO-US08656.

XX PR 18-APR-2000; 2000US-0552929.

XX PR 26-JAN-2001; 2001US-0770160.

XX PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Drmanac RT;
 XX WPI; 2001-611725/70.
 XX
 XX Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 XX
 XX Claim 20; Page 181; 765pp; English.
 XX
 XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AA029510-AAU33304 represent the amino acid
 XX sequences of novel human secreted proteins of the invention.
 XX
 SQ Sequence 124 AA;

Query Match 100.0%; Score 58; DB 22; Length 124;
 Best Local Similarity 100.0%; Pred. No. 0.0096;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||
 Db 39 LVVYPWTQRF 48

RESULT 14
 AA013066

ID AA013066 standard; Protein; 127 AA.

XX AA013066;

XX 06-NOV-2001 (first entry)

XX Human polypeptide SEQ ID NO 26958.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

XX WO200164835-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US04927.

XX 28-FEB-2000; 2000US-0515126.

PR 18-MAY-2000; 2000US-0577409.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514838/56.

DR N-PSDB; AA192997.

XX Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune

PT disorders -

XX
 PS Claim 20; SEQ ID NO 26958; 1399pp + Sequence Listing; English.

XX
 CC The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AA00010-AA013910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 127 AA;

Query Match 100.0%; Score 58; DB 22; Length 127;
 Best Local Similarity 100.0%; Pred. No. 0.0098;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10

|||||

Db 39 LVVYPWTQRF 48

RESULT 15

AA009585

ID AA009585 standard; Protein; 128 AA.

XX AA009585;

XX 06-NOV-2001 (first entry)

XX Human polypeptide SEQ ID NO 23477.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

XX WO200164835-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US04927.

XX 28-FEB-2000; 2000US-0515126.

PR 18-MAY-2000; 2000US-0577409.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514838/56.

DR N-PSDB; AA189516.

XX Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -

XX Claim 20; SEQ ID NO 23477; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AA00010-AA013910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The

CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 128 AA;

Query Match 100.0%; Score 58; DB 22; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTQRF 10
|
Db 39 LVVYPWTQRF 48

Search completed: February 24, 2003, 11:02:23
Job time : 36 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: February 24, 2003, 11:01:26 ; Search time 14 Seconds
(without alignments)
21.016 Million cell updates/sec

Title: US-09-147-490-1
Perfect score: 58
Sequence: 1 LVVVPWTFQRF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2.6/ptodata/1/1aa/PTUS-COMB.pep:*
6: /cgn2.6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	10	2	US-08-627-173-4
2	58	100.0	10	2	US-08-627-173-4
3	58	100.0	10	2	US-08-535-882A-4
4	58	100.0	10	2	US-08-535-882A-26
5	58	100.0	10	3	US-09-005-546-4
6	58	100.0	10	3	US-09-005-546-26
7	58	100.0	55	4	US-09-352-078-9
8	58	100.0	74	2	US-08-105-989-21
9	58	100.0	74	2	US-08-105-989-25
10	58	100.0	74	4	US-09-138-922-21
11	58	100.0	74	4	US-09-138-922-25
12	58	100.0	143	4	US-09-230-603-22
13	58	100.0	144	4	US-09-230-603-21
14	58	100.0	146	1	US-07-923-692C-10
15	58	100.0	146	1	US-08-170-095B-2
16	58	100.0	146	1	US-08-184-237-10
17	58	100.0	146	1	US-08-240-712-19
18	58	100.0	146	1	US-08-240-712-20
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21	58	100.0	146	1	US-08-240-712-23
22	58	100.0	146	1	US-08-240-712-24
23	58	100.0	146	1	US-08-240-712-28
24	58	100.0	146	1	US-08-396-866-2
25	58	100.0	146	1	US-08-443-890-19
26	58	100.0	146	1	US-08-443-890-20
27	58	100.0	146	1	US-08-443-890-21

28	58	100.0	146	1	US-08-443-890-22	Sequence 22, Appl
29	58	100.0	146	1	US-08-443-890-23	Sequence 23, Appl
30	58	100.0	146	1	US-08-443-890-24	Sequence 24, Appl
31	58	100.0	146	1	US-08-443-890-28	Sequence 28, Appl
32	58	100.0	146	2	US-08-484-686B-66	Sequence 66, Appl
33	58	100.0	146	2	US-08-484-686B-67	Sequence 67, Appl
34	58	100.0	146	2	US-08-484-686B-68	Sequence 68, Appl
35	58	100.0	146	2	US-08-484-686B-70	Sequence 70, Appl
36	58	100.0	146	2	US-08-432-071B-4	Sequence 4, Appl
37	58	100.0	146	2	US-08-627-173-18	Sequence 18, Appl
38	58	100.0	146	2	US-08-627-173-22	Sequence 22, Appl
39	58	100.0	146	2	US-08-482-920-10	Sequence 10, Appl
40	58	100.0	146	2	US-08-535-882A-18	Sequence 18, Appl
41	58	100.0	146	2	US-08-535-882A-22	Sequence 22, Appl
42	58	100.0	146	2	US-08-619-708A-6	Sequence 6, Appl
43	58	100.0	146	3	US-08-316-424A-4	Sequence 4, Appl
44	58	100.0	146	3	US-08-316-424A-8	Sequence 8, Appl
45	58	100.0	146	3	US-08-381-175A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-627-173-4
; Sequence 4, Application US/08627173
; Patent No. 5861483
; GENERAL INFORMATION:
; APPLICANT: TSYRLOVA, IRENA
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,173
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,882
; FILING DATE: 28-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1331-177
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-627-173-4

Query Match 100.0%; Score 58; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVVVPWTFQRF 10

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; COUNTRY: U.S.A.  

; ZIP: 22201-4714  

; COMPUTER READABLE FORM:  

; MEDIUM TYPE: Floppy disk  

; COMPUTER: IBM PC compatible  

; OPERATING SYSTEM: PC-DOS/MS-DOS  

; SOFTWARE: PatentIn Release #1.0, Version #1.30  

; CURRENT APPLICATION DATA:  

; APPLICATION NUMBER: US/08/535,882A  

; FILING DATE: 28-SEP-1995  

; CLASSIFICATION: 435  

; ATTORNEY/AGENT INFORMATION:  

; NAME: BYRNE, THOMAS E.  

; REGISTRATION NUMBER: 32,205  

; REFERENCE/DOCKET NUMBER: 1331-177  

; TELECOMMUNICATION INFORMATION:  

; TELEPHONE: (703) 816-4000  

; TELEFAX: (703) 816-4100  

; INFORMATION FOR SEQ ID NO: 4:  

; SEQUENCE CHARACTERISTICS:  

; LENGTH: 10 amino acids  

; TYPE: amino acid  

; STRANDEDNESS:  

; TOPOLOGY: linear  

; MOLECULE TYPE: peptide  

; US-08-535-882A-4  

Query Match 100.0%; Score 58; DB 2; Length 10;  

Best Local Similarity 100.0%; Pred. No. 0.0003;  

Matches 10; Conservative 0; Mismatches 0; Indels 0  

Qy 1 LVVYPWTQRF 10  

| | | | |  

Db 1 LVVYPWTQRF 10  

RESULT 4  

US-08-535-882A-26  

; Sequence 26, Application US/08535882A  

; Patent No. 5939391  

; GENERAL INFORMATION:  

; APPLICANT: TSYRLOVA, IRENA  

; APPLICANT: WOLPE, STEPHEN D.  

; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND  

; TITLE OF INVENTION: USES THEREOF  

; NUMBER OF SEQUENCES: 27  

; CORRESPONDENCE ADDRESS:  

; ADDRESSEE: NIXON & VANDERHYE P.C.  

; STREET: 1100 NORTH GLEBE ROAD  

; CITY: ARLINGTON  

; STATE: VIRGINIA  

; COUNTRY: U.S.A.  

; ZIP: 22201-4714  

; COMPUTER READABLE FORM:  

; MEDIUM TYPE: Floppy disk  

; COMPUTER: IBM PC compatible  

; OPERATING SYSTEM: PC-DOS/MS-DOS  

; SOFTWARE: PatentIn Release #1.0, Version #1.30  

; CURRENT APPLICATION DATA:  

; APPLICATION NUMBER: US/08/535,882A  

; FILING DATE: 28-SEP-1995  

; CLASSIFICATION: 435  

; ATTORNEY/AGENT INFORMATION:  

; NAME: BYRNE, THOMAS E.  

; REGISTRATION NUMBER: 32,205  

; REFERENCE/DOCKET NUMBER: 1331-177  

; TELECOMMUNICATION INFORMATION:  

; TELEPHONE: (703) 816-4000  

; TELEFAX: (703) 816-4100  

; INFORMATION FOR SEQ ID NO: 26:  

; SEQUENCE CHARACTERISTICS:  

; LENGTH: 10 amino acids  

; TYPE: amino acid  

; STRANDEDNESS:  

; TOPOLOGY: linear  

; MOLECULE TYPE: peptide  

; US-08-627-173-26  

Query Match 100.0%; Score 58; DB 2; Length 10;  

Best Local Similarity 100.0%; Pred. No. 0.0003;  

Matches 10; Conservative 0; Mismatches 0; Indels 0;  

Gaps 0;  

Qy 1 LVVYPWTQRF 10  

| | | | |  

Db 1 LVVYPWTQRF 10  

RESULT 3  

US-08-535-882A-4  

; Sequence 4, Application US/08535882A  

; Patent No. 5939391  

; GENERAL INFORMATION:  

; APPLICANT: TSYRLOVA, IRENA  

; APPLICANT: WOLPE, STEPHEN D.  

; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND  

; TITLE OF INVENTION: USES THEREOF  

; NUMBER OF SEQUENCES: 27  

; CORRESPONDENCE ADDRESS:  

; ADDRESSEE: NIXON & VANDERHYE P.C.  

; STREET: 1100 NORTH GLEBE ROAD  

; CITY: ARLINGTON  

; STATE: VIRGINIA

```



```
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-535-882A-26

Query Match      100.0%; Score 58; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. NO. 0.0003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
   | | | | | | | |
Db 1 LVVYPWTQRF 10

RESULT 5
US-09-005-546-4
; Sequence 4, Application US/09005546
; Patent No. 6090782
; GENERAL INFORMATION:
; APPLICANT: TSYRLOVA, IRENA
; APPLICANT: WOLPE, STEPHEN D.
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,546
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,882
; FILING DATE: 28-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1331-177
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-005-546-26

Query Match      100.0%; Score 58; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. NO. 0.0003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
   | | | | | | | |
Db 1 LVVYPWTQRF 10

RESULT 7
US-09-352-078-9
; Sequence 9, Application US/09352078
; Patent No. 6337314
; GENERAL INFORMATION:
; APPLICANT: Theragem, Inc.
; APPLICANT: Hoffmann, Brian F.
; APPLICANT: Dubnick, Bernard
; TITLE OF INVENTION: USE OF MAMMALIAN-DERIVED PEPTIDES FOR
; FILE REFERENCE: 1944/1D9990S1
; CURRENT APPLICATION NUMBER: US/09/352,078
; CURRENT FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: PCT/US98/16746
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/061,454
; EARLIER FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-352-078-9

QY 1 LVVYPWTQRF 10
   | | | | | | | |
Db 1 LVVYPWTQRF 10

RESULT 6
US-09-005-546-26
; Sequence 26, Application US/09005546
; Patent No. 6090782
; GENERAL INFORMATION:
```

Query Match 100.0%; Score 58; DB 4; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41

RESULT 8

US-08-105-989-21
; Sequence 21, Application US/08105989
; Patent No. 5922854
; GENERAL INFORMATION:
; APPLICANT: Kumar, Ramesh
; APPLICANT: Sharma, Ajay
; APPLICANT: Paulhiac, Clara
; APPLICANT: Khoury-Christianson, Anastasia P.
; TITLE OF INVENTION: Production of Human Hemoglobin in
; Transgenic Pigs.
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/105,989
; FILING DATE: 11-AUG-1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6794-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-105-989-21

Query Match 100.0%; Score 58; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 2 LVVYPWTQRF 11

RESULT 9

US-08-105-989-25
; Sequence 25, Application US/08105989
; Patent No. 5922854
; GENERAL INFORMATION:
; APPLICANT: Kumar, Ramesh
; APPLICANT: Sharma, Ajay
; APPLICANT: Paulhiac, Clara
; APPLICANT: Khoury-Christianson, Anastasia P.

; APPLICANT: Midha, Sunita
; TITLE OF INVENTION: Production of Human Hemoglobin in
; Transgenic Pigs.
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/105,989
; FILING DATE: 11-AUG-1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6794-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-105-989-25

Query Match 100.0%; Score 58; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 2 LVVYPWTQRF 11

RESULT 10

US-09-138-922-21
; Sequence 21, Application US/09138922
; Patent No. 6147202
; GENERAL INFORMATION:
; APPLICANT: Kumar, Ramesh
; APPLICANT: Sharma, Ajay
; APPLICANT: Paulhiac, Clara
; APPLICANT: Khoury-Christianson, Anastasia P.
; APPLICANT: Midha, Sunita
; TITLE OF INVENTION: Production of Human Hemoglobin in
; Transgenic Pigs.
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/138,922
; FILING DATE:

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/105,989
; FILING DATE: 11-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6794-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-138-922-21

Query Match 100.0%; Score 58; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 2 LVVYPWTQRF 11

RESULT 11
US-09-138-922-25
; Sequence 25, Application US/09138922
; Patent No. 6147202
; GENERAL INFORMATION:
; APPLICANT: Kumar, Ramesh
; APPLICANT: Sharma, Ajay
; APPLICANT: Paulhiac, Clara
; APPLICANT: Khoury-Christianson, Anastasia P.
; APPLICANT: Midha, Sunita
; TITLE OF INVENTION: Production of Human Hemoglobin in
; TITLE OF INVENTION: Transgenic Pigs.
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/138,922
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/105,989
; FILING DATE: 11-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6794-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-138-922-25

Query Match 100.0%; Score 58; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 2 LVVYPWTQRF 11

RESULT 12
US-09-230-603-22
; Sequence 22, Application US/09230603
; Patent No. 6171826
; GENERAL INFORMATION:
; APPLICANT: LEVINE, JOSEPH D
; APPLICANT: APOSTOL, ILYDOR A
; TITLE OF INVENTION: METHODS OF CONTROLLING BETA DIMER FORMATION IN
; TITLE OF INVENTION: HEMOGLOBIN
; FILE REFERENCE: BXTB3060
; CURRENT APPLICATION NUMBER: US/09/230,603
; CURRENT FILING DATE: 1999-05-14
; EARLIER APPLICATION NUMBER: PCT/US97/13564
; EARLIER FILING DATE: 1997-08-01
; EARLIER APPLICATION NUMBER: 60/023,211
; EARLIER FILING DATE: 1996-08-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: NON_TER
; LOCATION: (1)
; OTHER INFORMATION: the N-terminal methionine residue incorporated
; OTHER INFORMATION: during the translation initiation step is excised
; OTHER INFORMATION: during translation and is not present in the
; OTHER INFORMATION: mature polypeptide chain
; US-09-230-603-22

Query Match 100.0%; Score 58; DB 4; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 33 LVVYPWTQRF 42

RESULT 13
US-09-230-603-21
; Sequence 21, Application US/09230603
; Patent No. 6171826
; GENERAL INFORMATION:
; APPLICANT: LEVINE, JOSEPH D
; APPLICANT: APOSTOL, ILYDOR A
; TITLE OF INVENTION: METHODS OF CONTROLLING BETA DIMER FORMATION IN
; TITLE OF INVENTION: HEMOGLOBIN
; FILE REFERENCE: BXTB3060
; CURRENT APPLICATION NUMBER: US/09/230,603
; CURRENT FILING DATE: 1999-05-14
; EARLIER APPLICATION NUMBER: PCT/US97/13564
; EARLIER FILING DATE: 1997-08-01
; EARLIER APPLICATION NUMBER: 60/023,211
; EARLIER FILING DATE: 1996-08-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 144
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; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: NON_TER
; LOCATION: (1)
; OTHER INFORMATION: the N-terminal methionine residue incorporated
; OTHER INFORMATION: during the translation initiation step is excised
; OTHER INFORMATION: during the translation and is not present in the
; OTHER INFORMATION: mature polypeptide chain
US-09-230-603-21

Query Match          100.0%; Score 58; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 33 LVVYPWTQRF 42

RESULT 14
US-07-923-692C-10
; Sequence 10, Application US/07923692C
; Patent No. 5316931
; GENERAL INFORMATION:
; APPLICANT: Donson, Jon
; APPLICANT: Dawson, William O.
; APPLICANT: Grantham, George L.
; APPLICANT: Turpen, Thomas H.
; APPLICANT: Turpen, Ann Myers
; APPLICANT: Garger, Stephen J.
; APPLICANT: Grill, Laurence K.
; TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Limbach & Limbach
; STREET: 2001 Ferry Building
; CITY: San Francisco
; STATE: CAL
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/923,692C
; FILING DATE: 31-JUL-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,244
; FILING DATE: 22-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 641,617
; FILING DATE: 16-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 310,881
; FILING DATE: 17-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 160,766
; FILING DATE: 26-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 160,771
; FILING DATE: 26-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 347,637
; FILING DATE: 05-MAY-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 363,138
; FILING DATE: 08-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 219,279
; FILING DATE: 15-JUL-1988
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; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: BIOG-20121
; REFERENCE/DOCKET NUMBER: USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-433-4150
; TELEFAX: 415-433-8716
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-923-692C-10

Query Match          100.0%; Score 58; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41

RESULT 15
US-08-170-095B-2
; Sequence 2, Application US/08170095B
; Patent No. 5563254
; GENERAL INFORMATION:
; APPLICANT: Hoffman, Stephen J.
; APPLICANT: Nagai, Kiyoshi
; TITLE OF INVENTION: Blood Substitutes
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 2545 Central Avenue
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 Inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.0.1
; SOFTWARE: Microsoft Word 5.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170,095B
; FILING DATE: December 20, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5563254ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: Hoffman 2A/CONT2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-541-3322
; TELEFAX: 303-444-3013
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown to applicant
; MOLECULE TYPE: protein
; HYPOTHETICAL: no
US-08-170-095B-2

Query Match          100.0%; Score 58; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41
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Search completed: February 24, 2003, 11:04:13
Job time : 15 secs

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RESULT 2
US-09-977-577-15
; Sequence 15, Application US/09977577

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; Patent No. US20020155995A1
; GENERAL INFORMATION:
; APPLICANT: MOESTRUP, Soren
; APPLICANT: MOLLER, Holger J.
; TITLE OF INVENTION: THE FUNCTION OF A HAPTOGLOBIN-HAEMOGLOBIN RECEPTOR AND THE USES T
; FILE REFERENCE: MOESTRUP-1A
; CURRENT APPLICATION NUMBER: US/09/977,577
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: US 60/270,120
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: DK PA 2001 00039
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: DK PA 2000 01543
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-577-15

Query Match          100.0%; Score 58; DB 9; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41

RESULT 3
US-09-977-577-16
; Sequence 16, Application US/09977577
; Patent No. US20020155995A1
; GENERAL INFORMATION:
; APPLICANT: MOESTRUP, Soren
; APPLICANT: MOLLER, Holger J.
; TITLE OF INVENTION: THE FUNCTION OF A HAPTOGLOBIN-HAEMOGLOBIN RECEPTOR AND THE USES T
; FILE REFERENCE: MOESTRUP-1A
; CURRENT APPLICATION NUMBER: US/09/977,577
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: US 60/270,120
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: DK PA 2001 00039
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: DK PA 2000 01543
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-577-16

Query Match          100.0%; Score 58; DB 9; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41

RESULT 4
US-09-977-577-17
; Sequence 17, Application US/09977577
; Patent No. US20020155995A1
; GENERAL INFORMATION:
; APPLICANT: MOESTRUP, Soren
; APPLICANT: MOLLER, Holger J.
; TITLE OF INVENTION: THE FUNCTION OF A HAPTOGLOBIN-HAEMOGLOBIN RECEPTOR AND THE USES T
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; FILE REFERENCE: MOESTRUP-1A
; CURRENT APPLICATION NUMBER: US/09/977,577
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: US 60/270,120
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: DK PA 2001 00039
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: DK PA 2000 01543
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-577-17

Query Match          100.0%; Score 58; DB 9; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41

RESULT 5
US-09-977-577-20
; Sequence 20, Application US/09977577
; Patent No. US20020155995A1
; GENERAL INFORMATION:
; APPLICANT: MOESTRUP, Soren
; APPLICANT: MOLLER, Holger J.
; TITLE OF INVENTION: THE FUNCTION OF A HAPTOGLOBIN-HAEMOGLOBIN RECEPTOR AND THE USE
; FILE REFERENCE: MOESTRUP-1A
; CURRENT APPLICATION NUMBER: US/09/977,577
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: US 60/270,120
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: DK PA 2001 00039
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: DK PA 2000 01543
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-577-20

Query Match          100.0%; Score 58; DB 9; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41

RESULT 6
US-10-085-853-33
; Sequence 33, Application US/10085853
; Publication No. US20020194643A1
; GENERAL INFORMATION:
; APPLICANT: Merot, Bertrand
; APPLICANT: Dieryck, Wilfrid
; APPLICANT: Lenee, Philippe
; APPLICANT: Marden, Michael
; APPLICANT: Gruber, Veronique
; APPLICANT: Pagnier, Renee-Jossee
; APPLICANT: Baudino, Sylvie
; APPLICANT: Poyart, Claude
```


;; TITLE OF INVENTION: METHOD FOR PRODUCING HAEMIN PROTEINS USING PLANT
;; TITLE OF INVENTION: CELLS,
;; TITLE OF INVENTION: RESULTING PROTEINS AND PRODUCTS CONTAINING SAME
;; FILE REFERENCE: 8076.147USWO
;; CURRENT APPLICATION NUMBER: US/10/085,853
;; CURRENT FILING DATE: 2001-10-18
;; PRIOR APPLICATION NUMBER: 08/983,564
;; PRIOR FILING DATE: 1998-06-09
;; PRIOR APPLICATION NUMBER: PCT/FR96/01123
;; PRIOR FILING DATE: 1996-07-17
;; PRIOR APPLICATION NUMBER: 95/08615
;; PRIOR FILING DATE: 1995-07-17
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 33
;; LENGTH: 146
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-085-853-33

Query Match 100.0%; Score 58; DB 9; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41
|||||

RESULT 7
US-09-839-164-4
; Sequence 4, Application US/09839164
; Patent No. US20020098583A1
; GENERAL INFORMATION:
; APPLICANT: KOZLOV, VLADIMIR
; TSIRLOVA, IRENA
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
; USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8th FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/839,164
; FILING DATE: 23-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/477,668
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/316,424
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: PCT/US94/03349
; FILING DATE: 29-MAR-1994
; APPLICATION NUMBER: US 08/040,942
; FILING DATE: 31-MAR-1993
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-839-164-4

Query Match 100.0%; Score 58; DB 9; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41
|||||

RESULT 8
US-09-839-164-8
; Sequence 8, Application US/09839164
; Patent No. US20020098583A1
; GENERAL INFORMATION:
; APPLICANT: KOZLOV, VLADIMIR
; TSIRLOVA, IRENA
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
; USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8th FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/839,164
; FILING DATE: 23-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/477,668
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/316,424
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: PCT/US94/03349
; FILING DATE: 29-MAR-1994
; APPLICATION NUMBER: US 08/040,942
; FILING DATE: 31-MAR-1993
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-839-164-8

Query Match 100.0%; Score 58; DB 10; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41
|||||

RESULT 9
US-09-977-577-21
; Sequence 21, Application US/09977577
; Patent No. US2002015595A1
; GENERAL INFORMATION:
; APPLICANT: MOESTRUP, Soren
; APPLICANT: MOLLER, Holger J.
; TITLE OF INVENTION: THE FUNCTION OF A HAPTOGLOBIN-HAEMOGLOBIN RECEPTOR AND THE USE
; FILE REFERENCE: MOESTRUP-1A
US-09-839-164-4

;; CURRENT APPLICATION NUMBER: US/09/977,577
;; PRIOR FILING DATE: 2001-10-16
;; PRIOR APPLICATION NUMBER: US 60/270,120
;; PRIOR FILING DATE: 2001-02-22
;; PRIOR APPLICATION NUMBER: DK PA 2001 00039
;; PRIOR FILING DATE: 2001-01-11
;; PRIOR APPLICATION NUMBER: DK PA 2000 01543
;; PRIOR FILING DATE: 2000-10-16
;; NUMBER OF SEQ ID NOS: 25
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 21
;; LENGTH: 147
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (15)..(15)
;; OTHER INFORMATION: xaa is unknown
US-09-977-577-21

Query Match 100.0%; Score 58; DB 9; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 33 LVVYPWTQRF 42

RESULT 10

US-09-839-164-6
;; Sequence 6, Application US/09839164
;; Patent No. US20020098583A1
;; GENERAL INFORMATION:
;; APPLICANT: KOZLOV, VLADIMIR
;; TSYRLOVA, IRENA

;; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
;; USES THEREOF

;; NUMBER OF SEQUENCES: 11

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: NIXON & VANDERHYE P.C.

;; STREET: 1100 NORTH GLEBE ROAD, 8th FLOOR

;; CITY: ARLINGTON

;; STATE: VIRGINIA

;; COUNTRY: U.S.A.

;; ZIP: 22201-4714

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: 1.44 Mb diskette

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: MS Word

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/839,164

;; FILING DATE: 23-Apr-2001

;; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/477,668

;; FILING DATE: 07-JUN-1995

;; APPLICATION NUMBER: US 08/316,424

;; FILING DATE: 30-SEP-1994

;; APPLICATION NUMBER: PCT/US94/03349

;; FILING DATE: 29-MAR-1994

;; APPLICATION NUMBER: US 08/040,942

;; FILING DATE: 31-MAR-1993

;; INFORMATION FOR SEQ ID NO: 6:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 146 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: <Unknown>

;; TOPOLOGY: linear

;; MOLECULE TYPE: peptide

;; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-839-164-6

Query Match 94.8%; Score 55; DB 10; Length 146;
Best Local Similarity 90.0%; Pred. No. 0.019;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRY 41

RESULT 11

US-09-147-490-8

;; Sequence 8, Application US/09147490

;; Patent No. US20020147129A1

;; GENERAL INFORMATION:

;; APPLICANT: MENDELSON, FREDERICK A.O.

;; APPLICANT: CHAI, SIEW YEEN

;; APPLICANT: MOELLER, INGRID

;; APPLICANT: ALDRED, PETER G.

;; APPLICANT: SMITH, IAN A.

;; APPLICANT: LEW, REBECCA A.

;; TITLE OF INVENTION: NEUROACTIVE PEPTIDE

;; FILE REFERENCE: 016786/0215

;; CURRENT APPLICATION NUMBER: US/09/147,490

;; CURRENT FILING DATE: 1999-05-03

;; PRIOR APPLICATION NUMBER: PCT/AU97/00436

;; PRIOR FILING DATE: 1997-07-09

;; PRIOR APPLICATION NUMBER: AU P00893

;; PRIOR FILING DATE: 1996-07-09

;; NUMBER OF SEQ ID NOS: 10

;; SOFTWARE: PatentIn Ver. 2.1

;; SEQ ID NO 8

;; LENGTH: 147

;; TYPE: PRT

;; ORGANISM: Rattus sp.

US-09-147-490-8

Query Match 94.8%; Score 55; DB 10; Length 147;
Best Local Similarity 90.0%; Pred. No. 0.02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 33 LVVYPWTQRY 42

RESULT 12

US-09-826-290-201

;; Sequence 201, Application US/09826290

;; Patent No. US20020164668A1

;; GENERAL INFORMATION:

;; APPLICANT: Durham, L.Kathryn

;; APPLICANT: Friedman, David L.

;; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri

;; APPLICANT: Kimmel, Lida H.

;; APPLICANT: Parekh, Rajesh Bhikhu

;; APPLICANT: Potter, David M.

;; APPLICANT: Rohlf, Christian

;; APPLICANT: Silber, B. Michael

;; APPLICANT: Stiger, Thomas R.

;; APPLICANT: Sunderland, P. Trey

;; APPLICANT: Townsend, Robert Reid

;; APPLICANT: White, Frost

;; APPLICANT: Williams, Stephen A.

;; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and

;; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of

;; TITLE OF INVENTION: Alzheimer's Disease

;; FILE REFERENCE: 2572-1-001 N2

;; CURRENT APPLICATION NUMBER: US/09/826,290

;; CURRENT FILING DATE: 2001-04-30

;; PRIOR APPLICATION NUMBER: US 60/194,504

;; PRIOR FILING DATE: 2000-04-03

;; PRIOR APPLICATION NUMBER: US 60/253,647

; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-201

Query Match 89.7%; Score 52; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQR 9
| | | | | | | |
Db 2 LVVYPWTQR 10

RESULT 13

US-09-791-389-159
; Sequence 159, Application US/09791389
; Publication No. US20030032773A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N2
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US/09/791,389
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-159

Query Match 89.7%; Score 52; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQR 9
| | | | | | | |
Db 2 LVVYPWTQR 10

RESULT 14

US-09-791-393-159
; Sequence 159, Application US/09791393
; Publication No. US20030032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24

; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-393-159

Query Match 89.7%; Score 52; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQR 9
| | | | | | | |
Db 2 LVVYPWTQR 10

RESULT 15

US-09-791-378-251
; Sequence 251, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-061-999
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US/09/791,378
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 251
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-251

Query Match 89.7%; Score 52; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQR 9
| | | | | | | |
Db 2 LVVYPWTQR 10

Search completed: February 24, 2003, 11:04:31
Job time : 11 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 24, 2003, 11:01:22 ; Search time 47 Seconds
(without alignments)
20.454 Million cell updates/sec

Title: US-09-147-490-1
Perfect score: 58
Sequence: 1 LVVYPWTQRF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 2832224

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

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Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	58	100.0	61	4	I65317	hemoglobin delta c
2	58	100.0	61	4	I25202	hemoglobin beta ch
3	58	100.0	110	4	I46172	hypothetical hemog
4	58	100.0	122	2	A05304	hemoglobin beta-l
5	58	100.0	141	1	HGTC	hemoglobin beta-c
6	58	100.0	141	1	HMFCS	hemoglobin beta-C
7	58	100.0	141	1	HBSHCR	hemoglobin beta-C
8	58	100.0	142	1	HBSHC	hemoglobin beta-C
9	58	100.0	145	1	HBSOB	hemoglobin beta ch
10	58	100.0	145	1	HBSOBB	hemoglobin beta-A
11	58	100.0	145	1	HBSOG	hemoglobin beta ch
12	58	100.0	145	1	HBYA2	hemoglobin beta ch
13	58	100.0	145	1	HBSOKA	hemoglobin beta ch
14	58	100.0	145	1	HBEKN	hemoglobin beta ch
15	58	100.0	145	1	HBD3	hemoglobin beta-II
16	58	100.0	145	1	HBSHB	hemoglobin beta-B
17	58	100.0	145	1	HBSHA	hemoglobin beta-A
18	58	100.0	145	1	HBGTA	hemoglobin beta-A
19	58	100.0	145	1	HBGOF	hemoglobin beta ch
20	58	100.0	145	1	HGCTF	hemoglobin beta ch
21	58	100.0	145	1	HGSH	hemoglobin beta ch
22	58	100.0	145	2	B58794	hemoglobin beta ch
23	58	100.0	145	2	S13609	hemoglobin beta ch
24	58	100.0	145	2	C25727	hemoglobin beta ch
25	58	100.0	146	1	HBCZP	hemoglobin beta ch
26	58	100.0	146	1	HBSI	hemoglobin beta ch
27	58	100.0	146	1	HBMQP	hemoglobin beta ch
28	58	100.0	146	1	HBMQJ	hemoglobin beta ch
29	58	100.0	146	1	HBMQPM	hemoglobin beta ch

ALIGNMENTS

```

RESULT 1
I65317
hemoglobin delta chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 12-Jul-1996 #sequence-revision 31-Jul-1997 #text_change 20-Apr-2000
C:Accession: I65317
R:Liù, J.Z.; Harano, T.; Lancelos, K.D.; Huisman, T.H.
Biochim. Biophys. Acta 909, 208-212, 1987
A:Title: The beta-delta crossover leading to the beta delta hybrid gene of
A:Reference number: I52502; MUID:87299720; PMID:3620470
A:Accession: I65317
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-61 <LIU>
A:Cross-references: GB:M25661; NID:g183863; PIDN:AAA53154.1; PID:g183864
A>Note: this sequence was not determined in this report
C:Genetics:
A:Gene: GDB:HBD
A:Cross-references: GDB:l19298
A:Map position: llp15.5-llp15.5
A:Introns: 31/3

```

Query Match 100.0%; Score 58; DB 4; Length 61;
 Best Local Similarity 100.0%; Pred. No. 0.0037;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||

DB 33 LVVYPWTQRF 42
 |||||

RESULT 3

I46172

hypothetical hemoglobin psi-beta-2 pseudogene - goat (fragment)
 C:Species: Capra aegagrus hircus (domestic goat)
 C:Date: 21-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 19-May-2000
 C:Accession: I46172
 R:Cleary, M.L.; Schon, E.A.; Lingrel, J.B.
 Cell 26, 181-190, 1981

A:Title: Two related pseudogenes are the result of a gene duplication in the goat beta-globin gene
 A:Reference number: I46172; MUID:82137052; PMID:7332927

A:Accession: I46172

A>Status: translated from GB/EMBL/DBJ; conceptual translation of pseudogene

A:Molecule type: DNA

A:Residues: 1-110 <CLE>

A:Cross-references: EMBL:V00154; NID:9965; PIDN:CAA23469.1; PID:9966

C:Genetics:

A:Introns: 11/3; 18/3; 29/2; 103/3

C:Keywords: pseudogene

Query Match 100.0%; Score 58; DB 4; Length 110;

Best Local Similarity 100.0%; Pred. No. 0.0065;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||

DB 31 LVVYPWTQRF 40
 |||||

RESULT 4

A05304

hemoglobin beta-1 chain - Indian spiny-tailed lizard (tentative sequence) (fragments)

C:Species: Uromastix hardwickii (Indian spiny-tailed lizard)

C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000

C:Accession: A05304

R:Naqvi, S.; Zaidi, Z.H.; von Bahr-Lindstrom, H.; Carlquist, M.; Jornvall, H.

FEBS Lett. 162, 290-295, 1983

A:Reference number: A91314; MUID:84029159; PMID:6628672

A:Accession: A05304

A:Molecule type: protein

A:Residues: 1-122 <NAQ>

A:Note: the peptides were positioned by homology

C:Superfamily: globin; globin homology

C:Keywords: chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F:3-122/Domain: globin homology (fragments) <GLB>

F:80/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 2; Length 122;

Best Local Similarity 100.0%; Pred. No. 0.0072;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||

DB 32 LVVYPWTQRF 41
 |||||

RESULT 5

HBGTC

hemoglobin beta-C chain - goat

C:Species: Capra aegagrus hircus (domestic goat)

C:Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 03-Mar-2000

C:Accession: B02396; I46277; A02396

R:Schon, E.A.; Cleary, M.L.; Haynes, J.R.; Lingrel, J.B.

Cell 27, 359-369, 1981

A:Title: Structure and evolution of goat gamma-, beta(c)- and beta(A)-globin genes: t

A:Reference number: A90817; MUID:82137075; PMID:6277503

A:Accession: B02396

A:Molecule type: DNA

A:Residues: 1-141 <SCH>

A:Cross-references: GB:M15389

A:Note: Initiator Met not shown

R:Haynes, J.R.; Rosteck, P.R.; Schon, E.A.; Gallagher, P.M.; Burks, D.J.; Smith, K.;

J. Biol. Chem. 255, 6355-6367, 1980

A:Title: The isolation of the beta-a-, beta-c-, and gamma-globin genes and a presumed

A:Reference number: I46273; MUID:80227766; PMID:6248519

A:Accession: I46277

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 66-93, 'XX', '118-134 <HAY>

A:Cross-references: GB:K00662; NID:6164154; PID:6164158

C:Comment: This type of beta-C chain is found when anemia has been experimentally pro

C:Genetics:

A:Introns: 26/2; 100/3

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car

F:1-141/Domain: globin homology <GLB>

F:58/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:87/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 141;

Best Local Similarity 100.0%; Pred. No. 0.0083;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||

DB 27 LVVYPWTQRF 36
 |||||

RESULT 6

HBMEC

hemoglobin beta-C chain - mouflon (tentative sequence)

C:Species: Ovis orientalis musimon, Ovis ammon musimon (mouflon)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-2000

C:Accession: A90232; A02396

R:Wilson, J.B.; Miller, A.; Huisman, T.H.J.

Biochem. Genet. 4, 677-688, 1970

A:Title: Production of hemoglobin C in the mouflon (Ovis musimon pallas, 1811) and t

ptides from the beta(B) and beta (C) chains.

A:Reference number: A90232; MUID:71089262; PMID:5496230

A:Accession: A90232

A:Molecule type: protein

A:Residues: 1-141 <WIL>

A:Note: compositions of tryptic peptides were determined; positions 100-111 were sequ

C:Comment: This type of beta-C chain is found when anemia has been experimentally pro

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car

F:1-141/Domain: globin homology <GLB>

F:58/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:87/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 141;

Best Local Similarity 100.0%; Pred. No. 0.0083;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||

DB 27 LVVYPWTQRF 36
 |||||

RESULT 7

HBSHCR

hemoglobin beta-C chain - aoudad (tentative sequence)

C:Species: Ammotragus lervia (aoudad, Barbary sheep)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-2000

C:Accession: B90232; A02396

R:Wilson, J.B.; Miller, A.; Huisman, T.H.J.

Biochem. Genet. 4, 677-688, 1970

A;Title: Production of hemoglobin C in the moufflon (Ovis musimon pallas, 1811) and the ptides from the beta(B) and beta (C) chains.
A;Reference number: A90232; MUID:71089262; PMID:5496230
A;Accession: B90232
A:Molecule type: protein
A;Residues: 1-141 <WIL>
A;Note: compositions of tryptic peptides were determined; positions 100-111 were sequenced
C;Comment: This type of beta-C chain is found when anemia has been experimentally produced
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F:1-141/Domain: globin homology <GLB>
F:58/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:87/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTFQRF 10
|||||
Db 27 LVVYPWTFQRF 36

RESULT 8
HBSCC
hemoglobin beta-C chain - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 30-Sep-1993 #sequence.revision 30-Jan-1998 #text_change 03-Mar-2000
C;Accession: S10074; B92027; A90045; A02396
R;Garner, K.J.; Lingrel, J.B.
J. Mol. Evol. 28, 175-184, 1989
A;Title: A comparison of the beta(A)- and beta(B)-globin gene clusters of sheep.
A;Reference number: S10073; MUID:89178744; PMID:2494347
A;Accession: S10074
A:Molecule type: DNA
A;Residues: 1-142 <GAR>
A;Cross-references: EMBL:X14728; NID:g1212; PIDN:CAA32850.1; PID:g1213
A;Note: the authors translated the codon GTC for residue 30 as Ala
A;Note: the sequence of codons and residues 41-60 is repeated twice in the authors' translation
R;Boyer, S.H.; Hathaway, P.; Pascasio, F.; Bordley, J.; Orton, C.; Naughton, M.A.
J. Biol. Chem. 242, 2211-2232, 1967
A;Title: Differences in the amino acid sequences of tryptic peptides from three sheep hemoglobins
A;Reference number: A92027; MUID:67134347; PMID:6022868
A;Accession: B92027
A:Molecule type: protein
A;Residues: 2-64, 'B', 66-68, 'B', 70-71, 'Z', 73-74, 'BB', 77-82, 'Z', 84-85, 'Z', 87-94, 'B', 96, 'Z'
A;Experimental source: Dorset breed
R;Wilson, J.B.; Edwards, W.C.; McDaniel, M.; Dobbs, M.M.; Huismann, T.H.J.
Arch. Biochem. Biophys. 115, 385-400, 1966
A;Title: The structure of sheep hemoglobins. II. The amino acid composition of the tryptic peptides
A;Reference number: A90045
A;Accession: A90045
A:Molecule type: protein
A;Residues: 2-64, 'B', 66-68, 'B', 70-71, 'Z', 73-74, 'BB', 77-82, 'Z', 84-85, 'Z', 87-94, 'B', 96, 'Z'
A;Experimental source: Rambouillet breed
A;Note: there are several discrepancies between the sequence in this paper and that given in the literature
C;Comment: This beta-C chain is produced when anemia is experimentally induced.
C;Genetics:
A;Introns: 26/2; 100/3
C;Complex: Two beta chains combine to form heterotetramers with two alpha chains to form hemoglobin
C;Function:
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
F:1-142/Domain: globin homology <GLB>
F:2-142/Product: hemoglobin beta-C chain #status experimental <MAT>
F:59/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:88/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTFQRF 10
|||||
Db 28 LVVYPWTFQRF 37

RESULT 9
HBBOB
hemoglobin beta chain [validated] - bovine
N;Alternate names: hemoglobin-derived opioid peptide
N;Contains: LVV-hemorphin-7; VV-hemorphin-7
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Apr-1984 #sequence.revision 25-Feb-1985 #text_change 15-Sep-2000
C;Accession: B93504; A90046; B90046; A90052; B90052; S35696; S65609; A02387
R;Schimenti, J.C.; Duncan, C.H.
Nucleic Acids Res. 12, 1641-1655, 1984
A;Title: Ruminant globin gene structures suggest an evolutionary role for Alu-type repeats
A;Reference number: A93504; MUID:84144058; PMID:6322113
A;Accession: B93504
A:Molecule type: DNA
A;Residues: 1-145 <SCI>
A;Cross-references: EMBL:X00376; NID:g394; PIDN:CAA25111.1; PID:g395
A;Experimental source: beta A allele, Jersey cattle
R;Schroeder, W.A.; Shelton, J.R.; Shelton, J.B.; Robberson, B.; Babin, D.R.
Arch. Biochem. Biophys. 120, 124-135, 1967
A;Title: A comparison of amino acid sequences in the beta-chains of adult bovine hemoglobin
A;Reference number: A90046; MUID:68001834; PMID:6048711
A;Accession: A90046
A:Molecule type: protein
A;Residues: 1-145 <SCR1>
A;Experimental source: beta A allele, Jersey cattle
A;Accession: B90046
A:Molecule type: protein
A;Residues: 1-14, 'S', 16-17, 'H', 19-118, 'N', 120-145 <SCR2>
A;Experimental source: beta B allele, Jersey cattle
R;Schroeder, W.A.; Shelton, J.R.; Shelton, J.B.; Apell, G.; Huismann, T.H.J.; Smith, L.
Arch. Biochem. Biophys. 152, 222-232, 1972
A;Title: Amino acid sequences in the beta-chains of adult bovine hemoglobins C-Rhodes
A;Reference number: A90052; MUID:73007895; PMID:4561255
A;Accession: A90052
A:Molecule type: protein
A;Residues: 1-130, 'O', 132-145 <SCR3>
A;Experimental source: C-Rhodesia allele, Angoni cattle (East African short-horn zebu)
A;Accession: B90052
A:Molecule type: protein
A;Residues: 1-19, 'G', 21-42, 'T', 44-145 <SCR4>
A;Experimental source: B-Zambia allele, Angoni cattle (East African short-horn zebu)
R;Barkhudaryan, N.; Kellermann, J.; Galoyan, A.; Lottspeich, F.
FEBS Lett. 329, 215-218, 1993
A;Title: High molecular weight aspartic endopeptidase generates a coronaro-constrictor peptide
A;Reference number: S35696; MUID:93359052; PMID:8354398
A;Accession: S35696
A:Molecule type: protein
A;Residues: 31-40 <BAR>
A;Note: LVV-hemorphin-7 acts as a vasoconstrictor
R;Aubes-Dufau, I.; Capdevielle, J.; Seris, J.L.; Combes, D.
FEBS Lett. 364, 115-119, 1995
A;Title: Bitter peptide from hemoglobin hydrolysate: isolation and characterization.
A;Reference number: S65609; MUID:95269781; PMID:7750554
A;Accession: S65609
A:Molecule type: protein
A;Residues: 32-40 <AUB>
A;Note: VV-hemorphin-7 isolated from a hydrolysate has a bitter taste
R;Fermi, G.
Submitted to the Brookhaven Protein Data Bank, May 1993
A;Reference number: A52353; PDB:1LHDA
A;Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 1-145
R;Perutz, M.F.; Fermi, G.; Poyart, C.; Pagnier, J.; Kister, J.
J. Mol. Biol. 233, 536-545, 1993
A;Title: A novel allosteric mechanism in haemoglobin. Structure of bovine deoxyhaemoglobin
A;Reference number: A58463; MUID:94016570; PMID:8411160
A;Contents: annotation; X-ray crystallography, 2.2 angstroms
C;Genetics:

A: Introns: 28/2; 102/3
 C: Complex: Two beta chains combine to form heterotetramers with two alpha chains to form C: Function:
 C: Superfamily: globin; globin homology
 C: Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
 F: 2-145/Domain: globin homology <GLB>
 F: 31-40/Product: LVV-hemorphin-7 #status experimental <OPIA>
 F: 32-40/Product: VW-hemorphin-7 #status experimental <OPI9>
 F: 62/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F: 91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 0.0085;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||
 Db 31 LVVYPWTQRF 40

RESULT 10
 HBBBOB
 hemoglobin beta-A chain - banteng (tentative sequence)
 C: Species: Bos javanicus (banteng)
 C: Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 03-Mar-2000
 C: Accession: A02388
 R: Namikawa, T.; Takenaka, O.; Takahashi, K.
 Biochem. Genet. 21, 787-796, 1983
 A: Title: Hemoglobin Bali (bovine): beta(A)18(BL)lys -> His: one of the "missing links" B
 A: Reference number: A02388; MUID: 84023669; PMID: 6626147
 A: Accession: A02388
 A: Molecule type: protein
 A: Residues: 1-145 <NAM>
 A: Experimental source: Hereford breed
 A: Note: tryptic peptides were positioned by homology with the bovine sequence
 C: Superfamily: globin; globin homology
 C: Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
 F: 2-145/Domain: globin homology <GLB>
 F: 62/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F: 91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 0.0085;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||
 Db 31 LVVYPWTQRF 40

RESULT 11
 HBBOG
 hemoglobin beta chain - gayal
 C: Species: Bos gaurus frontalis (gayal)
 C: Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 03-Mar-2000
 C: Accession: A02389
 R: Lalithanthuanga, R.; Braunitzer, G.
 Hoppe-Seyler's Z. Physiol. Chem. 365, 737-741, 1984
 A: Title: Amino-acid sequence of gayal hemoglobin (Bos gaurus frontalis, Bovidae).
 A: Reference number: A91737; MUID: 85005246; PMID: 6479895
 A: Accession: A02389
 A: Molecule type: protein
 A: Residues: 1-145 <LAL>
 C: Superfamily: globin; globin homology
 C: Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
 F: 2-145/Domain: globin homology <GLB>
 F: 62/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F: 91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 0.0085;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10

|||||

Db 31 LVVYPWTQRF 40

RESULT 12

HBYA2

hemoglobin beta chain - yak

C: Species: Bos mutus grunniens (yak)

C: Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 03-Mar-2000

C: Accession: A02390

R: Lalithanthuanga, R.; Wiesner, H.; Braunitzer, G.

Biochem. Chem. Hoppe-Seyler 366, 63-68, 1985

A: Title: Studies on yak hemoglobin (Bos grunniens, Bovidae): structural basis for high

A: Reference number: A90689; MUID: 85225945; PMID: 4005038

A: Contents: beta-I and beta-II alleles

A: Accession: A02390

A: Molecule type: protein

A: Residues: 1-145 <THE>

A: Note: the sequence from the beta-I allele differs from that shown in having 49-Thr,

C: Comment: The beta-II allele is shown.

C: Superfamily: globin; globin homology

C: Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F: 2-145/Domain: globin homology <GLB>

F: 62/Binding site: oxygen (His) (distal axial ligand) #status predicted

F: 91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match

Best Local Similarity 100.0%; Score 58; DB 1; Length 145;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10

|||||

Db 31 LVVYPWTQRF 40

RESULT 13

HBBOKA

hemoglobin beta chain - greater kudu

C: Species: Tragelaphus strepsiceros (greater kudu)

C: Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 03-Mar-2000

C: Accession: A02391

R: Rodewald, K.; Wiesner, H.; Braunitzer, G.

Biochem. Chem. Hoppe-Seyler 366, 395-402, 1985

A: Title: Primary structure of the hemoglobins from the greater kudu antelope (Tragelaphus strepsiceros)

A: Reference number: A90684; MUID: 85279893; PMID: 4026993

A: Accession: A02391

A: Molecule type: protein

A: Residues: 1-145 <ROD>

A: Note: there are two alleles for the beta chain, one having the sequence shown and t

C: Superfamily: globin; globin homology

C: Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F: 2-145/Domain: globin homology <GLB>

F: 62/Binding site: oxygen (His) (distal axial ligand) #status predicted

F: 91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match

Best Local Similarity 100.0%; Score 58; DB 1; Length 145;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10

|||||

Db 31 LVVYPWTQRF 40

RESULT 14

HBEKN

hemoglobin beta chain - European moose

C: Species: Alces alces alces (European moose, elk)

C: Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 03-Mar-2000

C: Accession: A02392

R;Aschauer, H.; Wiesner, H.; Braunitzer, G.
Hoppe-Seyler's Z. Physiol. Chem. 365, 1323-1330, 1984
A;Title: Zur intrinsischen Sauerstoffaffinitaet: die Primaerstruktur eines weiteren Rums
A;Reference number: A91729; MUID:85078042; PMID:6510898

A;Accession: A02392
A;Molecule type: protein
A;Residues: 1-145 <ASC>
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F;2-145/Domain: globin homology <GLB>
F;62/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 145;

Best Local Similarity 100.0%; Pred. No. 0.0085;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10

|||||

Db 31 LVVYPWTQRF 40

RESULT 15

HBDE3

hemoglobin beta-III chain - Virginia white-tailed deer
C;Species: Odocoileus virginianus virginianus (Virginia white-tailed deer)
C;Date: 28-Feb-1986 #sequence_revision 28-Feb-1986 #text_change 03-Mar-2000
C;Accession: A02393

R;Shimizu, K.; Wong, S.C.; Wilson, J.B.; Lam, H.; Reynolds, A.E.; Singh, P.; Huisman, T.
Hemoglobin 7, 15-45, 1983

A;Title: The primary sequence of the beta chain of Hb type III of the Virginia white-tailed deer hemoglobins, types II, IV, V, and VII, and relationships between intermolecular con
A;Reference number: A02393; MUID:83185439; PMID:6841126

A;Accession: A02393

A;Molecule type: protein

A;Residues: 1-145 <SHI>

C;Comment: This chain is one of five beta chain alleles.

C;Superfamily: globin; globin homology

C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F;2-145/Domain: globin homology <GLB>

F;62/Binding site: oxygen (His) (distal axial ligand) #status predicted

F;91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 145;

Best Local Similarity 100.0%; Pred. No. 0.0085;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10

|||||

Db 31 LVVYPWTQRF 40

Search completed: February 24, 2003, 11:03:16

Job time : 47 secs

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OM protein - protein search, using sw model

Run on: February 24, 2003, 11:01:21 ; Search time 10 seconds
(without alignments)
41.476 Million cell updates/sec

Title: US-09-147-490-1
Perfect score: 58
Sequence: 1 LVVYPWTQRF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	58	100.0	60	1 HBE_MACEU	P81042 macropus eu
2	58	100.0	141	1 HBBC_CAPHI	P02078 capra hircu
3	58	100.0	141	1 HBBC_SHEEP	P02079 ovis aries
4	58	100.0	145	1 HBBA_BOSJA	P04346 bos javanic
5	58	100.0	145	1 HBBA_CAPHI	P02077 capra hircu
6	58	100.0	145	1 HBBC_BOVIN	P02081 bos taurus
7	58	100.0	145	1 HBBC_CAPHI	P02082 capra hircu
8	58	100.0	145	1 HBBC_SHEEP	P02083 ovis aries
9	58	100.0	145	1 HBB_ALCAA	P02073 alces alces
10	58	100.0	145	1 HBB_BISBO	P09422 bison bonas
11	58	100.0	145	1 HBB_BOSGF	P02071 bos gaurus
12	58	100.0	145	1 HBB_BOSMU	P02072 bos mutus g
13	58	100.0	145	1 HBB_BOVIN	P02070 bos taurus
14	58	100.0	145	1 HBB_ODOVI	P02074 odocoileus
15	58	100.0	145	1 HBB_OVIMU	P02076 ovis orient
16	58	100.0	145	1 HBB_RANTA	P21380 rangifer ta
17	58	100.0	145	1 HBB_SHEEP	P02075 ovis aries
18	58	100.0	145	1 HBB_TRAST	P04245 tragelaphus
19	58	100.0	146	1 HBBI_IGUIT	P18987 iguana igua
20	58	100.0	146	1 HBBI_SPHPU	P10060 sphenodon p
21	58	100.0	146	1 HBBI_TAPTE	P02064 tapirus ter
22	58	100.0	146	1 HBBI_UROHA	P18991 uromastix h
23	58	100.0	146	1 HBBI_PANLE	P18988 panthera le
24	58	100.0	146	1 HBBI_TAPTE	P02065 tapirus ter
25	58	100.0	146	1 HBB_AILUFU	P18982 ailurus ful
26	58	100.0	146	1 HBB_AILME	P18983 ailuropoda
27	58	100.0	146	1 HBB_ANTPA	P14388 antrozous p
28	58	100.0	146	1 HBB_AOTTR	P02035 aotus trivi
29	58	100.0	146	1 HBB_ATEGE	P02034 ateles geof
30	58	100.0	146	1 HBB_BALAC	P18984 balaeopter
31	58	100.0	146	1 HBB_CALAR	P18985 callithrix
32	58	100.0	146	1 HBB_CAVPO	P02095 cavia porce
33	58	100.0	146	1 HBB_CEBAL	P02040 cebus albif

34	58	100.0	146	1 HBB_CEBAP	P02041 cebus apell
35	58	100.0	146	1 HBB_CERAE	P02028 cercopithec
36	58	100.0	146	1 HBB_CERSI	P02066 ceratotheri
37	58	100.0	146	1 HBB_CERTO	P02031 cercocebus
38	58	100.0	146	1 HBB_COLBA	P02033 colobus bad
39	58	100.0	146	1 HBB_COLPO	P19885 colobus pol
40	58	100.0	146	1 HBB_CROCR	P19986 crocuta cro
41	58	100.0	146	1 HBB_CTEGU	P20855 ctenodactyl
42	58	100.0	146	1 HBB_CYNBP	P11754 cynopterus
43	58	100.0	146	1 HBB_DASNO	P02087 dasyopus nov
44	58	100.0	146	1 HBB_ECHTE	P24292 echinops te
45	58	100.0	146	1 HBB_EQUHE	P02063 equus hemio

ALIGNMENTS

RESULT 1
HBE_MACEU
ID HBE_MACEU STANDARD; PRT; 60 AA.
AC P81042;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hemoglobin epsilon chain (Fragment).
GN HBE1.
OS Macropus eugenii (Tamar wallaby).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315;
RN [1]
RP SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=98000287; PubMed=9342240;
RA Holland R.A.B., Gocley A.A.;
RT "Characterization of the embryonic globin chains of the marsupial Tamar wallaby, Macropus eugenii.";
RL Eur. J. Biochem. 248:864-871(1997).
CC -!- FUNCTION: HEMOGLOBIN EPSILON CHAIN IS A EMBRYONIC-TYPE BETA-TYPE CHAIN FOUND IN PRENATAL AND NEONATAL MARSUPIALS.
CC -!- TISSUE SPECIFICITY: Red blood cells.
CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR HSSP; P02100; 1A9W.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Erythrocyte.
FT NON_TER 60
SQ SEQUENCE 60 AA; 6510 MW; C3CF20BC445C649C CRC64;

Query Match 100.0%; Score 58; DB 1; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
| | | | | | | | | |
DB 32 LVVYPWTQRF 41

RESULT 2
HBBC_CAPHI
ID HBBC_CAPHI STANDARD; PRT; 141 AA.
AC P02078;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta-C chain (Cysteine-beta).
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX NCBI_TaxID=9925;
RN [1]

```

RP SEQUENCE FROM N.A.
RX MEDLINE=82137075; PubMed=6277503;
RA Schon E.A., Cleary M.L., Haynes J.R., Lingrel J.B.;
RT "Structure and evolution of goat gamma-, beta C- and beta A-globin
RT genes: three developmentally regulated genes contain inserted
RT elements.";
RL Cell 27:359-369(1981).
CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC -!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -!- MISCELLANEOUS: THIS TYPE OF BETA-C CHAIN IS FOUND WHEN ANEMIA HAS
CC BEEN EXPERIMENTALLY PRODUCED.
CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
CC -----
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CC -----
DR EMBL; M15389; AAA30914.1; ALT_SEQ.
DR PIR; A02396; HBGTC.
DR HSSP; P02070; IFSX.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
DR Heme; Oxygen transport; Transport; Erythrocyte.
FT INIT_MET 0
FT METAL 58 58 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 141 AA; 15620 MW; 305CEA482FAC825C CRC64;

Query Match 100.0%; Score 58; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 27 LVVYPWTQRF 36

RESULT 3
HBBC_SHEEP STANDARD; PRT; 141 AA.
AC P02079;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hemoglobin beta-C chain.
OS Ovis aries (Sheep),
OS Ovis orientalis musimon (Mouflon), and
OS Ammotragus lervia (Barbary sheep) (Aoudad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis;
OX NCBI_TaxID=9940, 9938, 9899;
[1]
RP SEQUENCE FROM N.A.
RX SPECIES=Sheep;
RX MEDLINE=89178744; PubMed=2494347;
RA Garner K.J., Lingrel J.B.;
RT "A comparison of the beta A- and beta B-globin gene clusters of
RT sheep.";
RL J. Mol. Evol. 28:175-184(1989).
[2]
RP SEQUENCE.
RC SPECIES=Sheep;
RC MEDLINE=67134347; PubMed=6022868;
RX "The structure of sheep hemoglobins. II. The amino acid composition
of the tryptic peptides of the non-alpha chains of hemoglobins A, B,
C, and F.";
RL Arch. Biochem. Biophys. 115:385-400(1966).
[4]
COMPOSITION OF TRYPTIC PEPTIDES EXCEPT POSITIONS 100-111.
RC SPECIES=O.o.musimon, and A.lervia;
RX MEDLINE=71089262; PubMed=5496230;
RA Wilson J.B., Miller A., Huisman T.H.J.;
RT "Production of hemoglobin C in the Mouflon (Ovis musimon Pallas,
RT 1811) and the Barbary sheep (Ammotragus lervia Pallas, 1777) during
RT experimental anemia: amino acid composition of tryptic peptides from
RT the beta B and beta C chains.";
RL Biochem. Genet. 4:677-688(1970).
CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC -!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -!- MISCELLANEOUS: THIS TYPE OF BETA-C CHAIN IS FOUND IN THESE ANIMALS
CC WHEN ANEMIA HAS BEEN EXPERIMENTALLY PRODUCED.
CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X14728; CAA32850.1; -.
DR PIR; A02396; HBSHC.
DR PIR; A02396; HBSHCR.
DR PIR; S10074; S10074.
DR HSSP; P02070; IFSX.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
DR Heme; Oxygen transport; Transport; Erythrocyte.
FT INIT_MET 0
FT METAL 58 58 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 141 AA; 15619 MW; 3409EDB54528C358 CRC64;

Query Match 100.0%; Score 58; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 27 LVVYPWTQRF 36

RESULT 4
HBBA_BOSJA STANDARD; PRT; 145 AA.
ID HBBA_BOSJA
AC P04346;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)

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DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hemoglobin beta-A chain.
 OS Bos javanicus (Wild banteng).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9906;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=84023669; PubMed=6626147;
 RA Namikawa T., Takenaka O., Takahashi K.;
 RT "Hemoglobin Ball (bovine): beta A 18(B1)Lys leads to His: one of the
 RT 'missing links' between beta A and beta B of domestic cattle exists
 RT in the Bali cattle (Bovinae, Bos banteng).";
 RL Biochem. Genet. 21:787-796(1983).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A02388; HBB0BB.
 DR HSSP: P02070; IFSX.
 DR InterPro: IPR002337; Beta_haem.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transprot; Erythrocyte.
 FT METAL 62 IRON (HEME DISTAL LIGAND).
 FT METAL 91 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 145 AA; 15964 MW; 52685BDC8CFBDD5 CRC64;
 Query Match 100.0%; Score 58; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 0.0049;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LVVYPWTQRF 10
 Db 31 LVVYPWTQRF 40
 RESULT 5
 ID HBBA_CAPHI STANDARD; PRT; 145 AA.
 AC P02077;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Hemoglobin beta-A chain (Alanine-beta).
 OS Capra hircus (Goat).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82137075; PubMed=6277503;
 RA Schon E.A., Cleary M.L., Haynes J.R., Lingrel J.B.;
 RT "Structure and evolution of goat gamma-, beta C- and beta A-globin
 RT genes: three developmentally regulated genes contain inserted
 RT elements";
 RL Cell 27:359-369(1981).
 RN [2]
 RP PARTIAL SEQUENCE (ALLELE A).
 RX MEDLINE=67165362; PubMed=6026247;
 RA Huisman T.H.J., Adams H.R., Dimmock M.O., Edwards W.E., Wilson J.B.;
 RT "The structure of goat hemoglobins. I. Structural studies of the beta
 RT chains of the hemoglobins of normal and anemic goats.";
 RL J. Biol. Chem. 242:2534-2541(1967).
 RN [3]
 RP PARTIAL SEQUENCE (ALLELE D).
 RX MEDLINE=69036192; PubMed=5697993;
 RA Adams H.R., Boyd E.M., Wilson J.B., Miller A., Huisman T.H.J.;

RT "The structure of goat hemoglobins. 3. Hemoglobin D, a beta chain
 RT variant with one eparet amino acid substitution (21 Asp->His).";
 RL Arch. Biochem. Biophys. 127:398-405(1968).
 RN [4]
 RP PARTIAL SEQUENCE (ALLELE E).
 RX MEDLINE=70252721; PubMed=5433580;
 RA Wrightstone R.N., Wilson J.B., Miller A., Huisman T.H.J.;
 RT "The structure of goat hemoglobins. IV. A third beta chain variant
 RT (betaE) with three apparent amino acid substitutions.";
 RL Arch. Biochem. Biophys. 138:451-456(1970).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- POLYMORPHISM: THERE ARE AT LEAST ALLELES. THE SEQUENCE SHOWN IS
 CC THAT OF ALLELE A.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
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 CC or send an email to license@isb-sib.ch).
 DR EMBL: M15387; AAA30913.1;
 DR PIR: A02395; HBGTA.
 DR HSSP: P02070; IFSX.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transprot; Erythrocyte;
 KW Polymorphism.
 FT METAL 62 IRON (HEME DISTAL LIGAND).
 FT METAL 91 IRON (HEME PROXIMAL LIGAND).
 FT VARIANT 20 20 D -> H (IN ALLELE D).
 FT VARIANT 86 86 Q -> H (IN ALLELE E).
 FT VARIANT 103 103 K -> R (IN ALLELE E).
 FT VARIANT 124 124 L -> V (IN ALLELE E).
 SQ SEQUENCE 145 AA; 16021 MW; 6C59F105A940F4D0 CRC64;
 Query Match 100.0%; Score 58; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 0.0049;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LVVYPWTQRF 10
 Db 31 LVVYPWTQRF 40
 RESULT 6
 ID HBBF_BOVIN STANDARD; PRT; 145 AA.
 AC P02081;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta fetal chain (Hemoglobin gamma chain).
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84144058; PubMed=6322113;
 RA Schimmenti J.C., Durcan C.H.;
 RT "Ruminant globin gene structures suggest an evolutionary role for
 RT Alu-type repeats.";
 RL Nucleic Acids Res. 12:1641-1655(1984).

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RN  [2]
RX  MEDLINE=67089183; PubMed=5958205;
RA  Babin D.R., Schroeder W.A., Shelton J.R., Shelton J.B., Robberson B.;
RT  "The amino acid sequence of the gamma chain of bovine fetal
RL  hemoglobin.";
RL  Biochemistry 5:1297-1310(1966).
CC  -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC  -!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC  -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC  -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X00354; CAA25101.1; -
DR  EMBL; M63452; AAA30519.1; -
DR  PIR; A02398; HBBOF.
DR  HSSP; P02070; IFSX.
DR  InterPro; IPR002337; Beta_haem.
DR  InterPro; IPR000971; Globin.
DR  Pfam; PF00042; globin; 1.
DR  PRINTS; PR00814; BETAHAEM.
DR  PROSITE; PS01033; GLOBIN; 1.
KW  Heme; Oxygen transport; Transports; Erythrocyte.
FT  METAL 62 62 IRON (HEME DISTAL LIGAND).
FT  METAL 91 91 IRON (HEME PROXIMAL LIGAND).
SQ  SEQUENCE 145 AA; 15859 MW; 78B8722915E9C221 CRC64;

Query Match 100.0%; Score 58; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 31 LVVYPWTQRF 40
|||||
|

RESULT 7
HBBF_CAPHI
ID HBBF_CAPHI STANDARD; PRT; 145 AA.
AC P02082;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta fetal chain (Hemoglobin gamma chain).
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82137075; PubMed=6277503;
RA Schon E.A., Cleary M.L., Haynes J.R., Lingrel J.B.;
RT "Structure and evolution of goat gamma-, beta C- and beta A-globin
RT genes: three developmentally regulated genes contain inserted
RT elements.";
RL Cell 27:359-369(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=83005406; PubMed=7118074;
RA Kleinschmidt T., Braunitzer G.;
RT "The primary structure of the hemoglobin gamma-chains of fetal sheep
RT (Ovis ammon) and goat (Capra aegagrus), Artiodactyla.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:789-796(1982).
RN [3]

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RP  [2]
RX  MEDLINE=80227766; PubMed=6248519;
RA  Haynes J.R., Rosteck P.R., Schon E.A., Gallagher P.M., Burks D.J.,
RA  Smith K., Lingrel J.B.;
RT  "The isolation of the beta A-, beta C-, and gamma-globin genes and a
RT  presumptive embryonic globin gene from a goat DNA recombinant
RL  library.";
RL  J. Biol. Chem. 255:6355-6367(1980).
CC  -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC  -!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC  -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC  -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; M15388; AAA30925.1; -
DR  EMBL; K00663; AAA30923.1; -
DR  PIR; A02399; HBGTF.
DR  HSSP; P02070; IFSX.
DR  InterPro; IPR002337; Beta_haem.
DR  InterPro; IPR000971; Globin.
DR  Pfam; PF00042; globin; 1.
DR  PRINTS; PR00814; BETAHAEM.
DR  PROSITE; PS01033; GLOBIN; 1.
KW  Heme; Oxygen transport; Transports; Erythrocyte.
FT  METAL 62 62 IRON (HEME DISTAL LIGAND).
FT  METAL 91 91 IRON (HEME PROXIMAL LIGAND).
SQ  SEQUENCE 145 AA; 15946 MW; E143C91CC8989652 CRC64;

Query Match 100.0%; Score 58; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 31 LVVYPWTQRF 40
|||||
|

RESULT 8
HBBF_SHEEP
ID HBBF_SHEEP STANDARD; PRT; 145 AA.
AC P02083;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hemoglobin beta fetal chain (Hemoglobin gamma chain).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE OF 1-29; 52-96 AND 104-145 FROM N.A.
RX MEDLINE=8117290; PubMed=6161931;
RA Kretschmer P.J., Coon H.C., Davis A., Harrison M., Nienhuis A.W.;
RT "Hemoglobin switching in sheep. Isolation of the fetal gamma-globin
RT gene and demonstration that the fetal gamma- and adult beta A-globin
RT genes lie within eight kilobase segments of homologous DNA.";
RL J. Biol. Chem. 256:1975-1982(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=77022158; PubMed=974104;
RA Darbre P.D., Lehmann H.;
RT "The gamma chain of the lamb.";
RL Blochim. Biophys. Acta 446:10-18(1976).
CC  -!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.

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CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
CC -----
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CC -----
DR EMBL; K02824; AAA31533.1; -
DR EMBL; K02825; AAA31534.1; -
DR EMBL; K02826; AAA31535.1; -
DR PIR; A92306; HGSH.
DR HSP; P02070; IFSX.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 62 62 IRON (HEME DISTAL LIGAND).
FT METAL 91 91 IRON (HEME PROXIMAL LIGAND).
FT CONFLICT 119 120 GE -> EG (IN REF. 2).
SQ SEQUENCE 145 AA; 15931 MW; 9924A27CCBC34C28 CRC64;

Query Match 100.0%; Score 58; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTFQRF 10
Db 31 LVVYPWTFQRF 40
|||||

RESULT 9
HBB_ALCAA
ID HBB_ALCAA STANDARD; PRT; 145 AA.
AC P02073;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB.
OS Alces alces alces (European moose) (Elk).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Odocoileinae; Alces.
OX NCBI_TaxID=9853;
RN [1]
RP SEQUENCE.
RX MEDLINE=85078042; PubMed=6510898;
RA Aschauer H., Wiesner H., Braunitzer G.;
RT "Intrinsic oxygen affinity: the primary structure of a ruminantia
RT hemoglobin: methionine in betaNA2 of a pecora, the Northern elk
RL Hoppe-Seyler's Z. Physiol. Chem. 365:1323-1330(1984).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR; C25727; C25727.
DR HSP; P02070; IFSX.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 62 62 IRON (HEME DISTAL LIGAND).
FT METAL 91 91 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 145 AA; 16223 MW; C2D22F363D3B78EA CRC64;

Query Match 100.0%; Score 58; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTFQRF 10
Db 31 LVVYPWTFQRF 40
|||||

RESULT 9
HBB_ALCAA
ID HBB_ALCAA STANDARD; PRT; 145 AA.
AC P02073;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB.
OS Alces alces alces (European moose) (Elk).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Odocoileinae; Alces.
OX NCBI_TaxID=9853;
RN [1]
RP SEQUENCE.
RX MEDLINE=85078042; PubMed=6510898;
RA Aschauer H., Wiesner H., Braunitzer G.;
RT "Intrinsic oxygen affinity: the primary structure of a ruminantia
RT hemoglobin: methionine in betaNA2 of a pecora, the Northern elk
RL Hoppe-Seyler's Z. Physiol. Chem. 365:1323-1330(1984).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR; A02392; HBEKN.
DR HSP; P02070; IFSX.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 62 62 IRON (HEME DISTAL LIGAND).
FT METAL 91 91 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 145 AA; 16223 MW; C2D22F363D3B78EA CRC64;

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Query Match 100.0%; Score 58; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTFQRF 10
Db 31 LVVYPWTFQRF 40
|||||

RESULT 10
HBB_BISBO
ID HBB_BISBO STANDARD; PRT; 145 AA.
AC P09422;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB.
OS Bison bonasus (European bison).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Bovinae; Bison.
OX NCBI_TaxID=9902;
RN [1]
RP SEQUENCE.
RX MEDLINE=86296178; PubMed=3741621;
RA Mazur G., Mueller E., Braunitzer G., Wiesner H.;
RT "Intrinsic oxygen affinity of hemoglobins: the hemoglobin of bisons
RT (Bison bonasus,Bovidae).";
RL Biol. Chem. Hoppe-Seyler 367:417-423(1986).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR; C25727; C25727.
DR HSP; P02070; IFSX.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 62 62 IRON (HEME DISTAL LIGAND).
FT METAL 91 91 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 145 AA; 15976 MW; 4634F52EC1772BA3 CRC64;

Query Match 100.0%; Score 58; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTFQRF 10
Db 31 LVVYPWTFQRF 40
|||||

RESULT 11
HBB_BOSGF
ID HBB_BOSGF STANDARD; PRT; 145 AA.
AC P02071;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB.
OS Bos gaurus frontalis (Gaval), and
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=30520, 89462;
RN [1]

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RP SEQUENCE.
RC SPECIES=B.g.frontalis;
RX MEDLINE=85005246; PubMed=6479895;
RA Lalthantluanga R., Braunitzer G.;
RT "Amino-acid sequence of gaval hemoglobin (Bos gaurus frontalis, Bovidae).";
RL Hoppe-Seyler's Z. Physiol. Chem. 365:737-741(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=B.bubalis;
RX MEDLINE=92362189; PubMed=1499282;
RA Ferranti P., di Luccia A., Malorni A., Pucci P., Ruoppolo M., Marino G., Ferrara L.;
RT "River buffalo (Bubalus bubalis L.) AA phenotype haemoglobins: characterization by immobilized polyacrylamide gel electrophoresis and high performance liquid chromatography and determination of the primary structure of the constitutive chains by mass spectrometry.";
RL Comp. Biochem. Physiol. 101B:91-98(1992).
CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
CC -!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR: A02389; HBBG.
DR PIR: A49141; A49141.
DR HSSP; P02070; IFSX.
DR InterPro: IPR002337; Beta.haem.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transports; Erythrocyte.
FT METAL 62 IRON (HEME DISTAL LIGAND).
FT METAL 91 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 145 AA; 15986 MW; 5260F17E84737FB3 CRC64;

Query Match 100.0%; Score 58; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
DB 31 LVVYPWTQRF 40

RESULT 12
HBB_BOSMU
ID HBB_BOSMU STANDARD; PRT; 145 AA.
AC P02072;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB.
OS Bos mutus grunniens (Yak).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=30521;
RN [1]
RP SEQUENCE (BETA-I AND BETA-II ALLELES).
RX MEDLINE=85225945; PubMed=4005038;
RA Lalthantluanga R., Wiesner H., Braunitzer G.;
RT "Studies on yak hemoglobin (Bos grunniens, Bovidae): structural basis for high intrinsic oxygen affinity?";
RL Biol. Chem. Hoppe-Seyler 366:63-68(1985).
CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
CC -!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -!- POLYMORPHISM: THE BETA-II ALLELE IS SHOWN, IT OCCURS MUCH MORE FREQUENTLY THAN THE BETA-I ALLELE.
CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

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DR PIR: A02390; HBYA2.
DR HSSP; P02070; IFSX.
DR InterPro: IPR002337; Beta.haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transports; Erythrocyte.
KW Polymorphism.
FT METAL 62 IRON (HEME DISTAL LIGAND).
FT METAL 91 IRON (HEME PROXIMAL LIGAND).
FT VARIANT 49 49 S -> T (IN BETA-I ALLELE).
FT VARIANT 116 116 H -> N (IN BETA-I ALLELE).
FT VARIANT 134 134 V -> A (IN BETA-I ALLELE).
SQ SEQUENCE 145 AA; 15991 MW; F937353D4A65FAA2 CRC64;

Query Match 100.0%; Score 58; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
DB 31 LVVYPWTQRF 40

RESULT 13
HBB_BOVIN
ID HBB_BOVIN STANDARD; PRT; 145 AA.
AC P02070;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hemoglobin beta chain.
GN HBB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. (ALLELE A).
RX MEDLINE=84144058; PubMed=6322113;
RA Schimmenti J.C., Duncan C.H.;
RT "Ruminant globin gene structures suggest an evolutionary role for Alu-type repeats.";
RL Nucleic Acids Res. 12:1641-1655(1984).
RN [2]
RP SEQUENCE (ALLELES A AND B).
RX MEDLINE=68001834; PubMed=6048711;
RA Schroeder W.A., Shelton J.R., Shelton J.B., Robberson B., Babin D.R.;
RT "A comparison of amino acid sequences in the beta-chains of adult bovine hemoglobins A and B.";
RL Arch. Biochem. Biophys. 120:124-135(1967).
RN [3]
RP PARTIAL SEQUENCE (ALLELES C-RHODESIA AND D-ZAMBIA).
RX MEDLINE=73007895; PubMed=4561255;
RA Schroeder W.A., Shelton J.R., Shelton J.B., Apell G., Huisman T.H.J., Smith L.L., Carr W.R.;
RT "Amino acid sequences in the beta-chains of adult bovine hemoglobins C-Rhodesia and D-Zambia.";
RL Arch. Biochem. Biophys. 152:222-232(1972).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=94016570; PubMed=8411160;
RA Perutz M.F., Fermi G., Poyart C., Pagnier J., Kister J.;
RT "A novel allosteric mechanism in haemoglobin. Structure of bovine deoxyhaemoglobin, absence of specific chloride-binding sites and origin of the chloride-linked Bohr effect in bovine and human haemoglobin.";
RL J. Mol. Biol. 233:536-545(1993).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX MEDLINE=21262557; PubMed=11369847;

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RA Safo M.K., Abraham D.J.;
 RT "The x-ray structure determination of bovine carbonmonoxy hemoglobin
 at 2.1 Å resolution and its relationship to the quaternary structures
 of other hemoglobin crystal forms.";
 RL Protein Sci. 10:1091-1099(2001).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- POLYMORPHISM: FOUR ALLELIC BETA CHAINS HAVE BEEN FOUND IN BOVINE
 CC HEMOGLOBINS. A AND B ALLELES WERE FOUND IN JERSEY CATTLE AND C
 CC AND D ALLELES WERE FOUND IN ANGONI CATTLE (EAST AFRICAN SHORT-HORN
 CC ZEBU). THE SEQUENCE SHOWN IS THAT OF THE ALLELE A.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 CC -1- DATABASE: NAME=worthington enzyme manual;
 CC WWW="http://www.worthington-biochem.com/manual/H/HB.html".
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; X00376; CAA25111.1; -;
 DR EMBL; M63453; AAA30408.1; -;
 DR PIR; A02387; HBB0B.
 DR PDB; 1HDA; 31-MAY-94.
 DR PDB; 1FSX; 06-JUN-00.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PR00814; BETAHAEM.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte;
 KW Polymorphism; 3d-structure.
 FT METAL 62 62 IRON (HEME DISTAL LIGAND).
 FT METAL 91 91 IRON (HEME PROXIMAL LIGAND).
 FT VARIANT 15 15 G -> S (IN ALLELE B).
 FT VARIANT 18 18 K -> H (IN ALLELE B).
 FT VARIANT 20 20 D -> G (IN ALLELE D-ZAMBIA).
 FT VARIANT 43 43 S -> T (IN ALLELE D-ZAMBIA).
 FT VARIANT 119 119 K -> N (IN ALLELE B).
 FT VARIANT 131 131 K -> Q (IN ALLELE C-RHODESIA).
 SQ SEQUENCE 145 AA; 15954 MW; FD62217E8477CFD4 CRC64;
 Query Match 100.0%; Score 58; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 0.0049;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPWTQRF 10
 Db 31 LVVYPWTQRF 40
 RESULT 14
 HBB_ODOVI STANDARD; PRT; 145 AA.
 AC P02074;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hemoglobin beta-III chain.
 GN HBB.
 OS Odocoileus virginianus virginianus (Virginia white-tailed deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
 OC Cervidae; Odocoileinae; Odocoileus.
 OX NCBI_TaxID=9875;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=83185439; PubMed=6841126;

RA Shimizu K., Wong S.C., Wilson J.B., Lam H., Reynolds A.E., Singh P.,
 RA Huismann T.H.J., Charles N.G., Amma E.L.;
 RT "The primary sequence of the beta chain of Hb type III of the
 RT Virginia white-tailed deer (Odocoileus virginianus), a comparison with
 RT putative sequences of the beta chains from four additional deer
 RT hemoglobins, types II, IV, V, and VIII, and relationships between
 RT intermolecular contacts, primary sequence and sickling of deer
 RT hemoglobins.";
 RL Hemoglobin 7:15-45(1983).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.98 ÅNGSTROMS).
 RA Schmidt W.C. Jr., Gilling R.L., Houston T.E., Sproul G.D., Amma E.L.,
 RA Huismann T.H.J.;
 RT "The structure of sickling deer type III hemoglobin by molecular
 RT replacement.";
 RL Acta Crystallogr. B 33:335-342(1977).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- POLYMORPHISM: THIS CHAIN IS ONE OF FIVE BETA CHAIN ALLELES.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 CC -1- CAUTION: THERE ARE CONFLICTS WITH THE SEQUENCE STORED IN PDB.
 DR PIR; A02393; HBDE3.
 DR PDB; 1HDS; 30-SEP-83.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PR00814; BETAHAEM.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte;
 KW 3d-structure.
 FT METAL 62 62 IRON (HEME DISTAL LIGAND).
 FT METAL 91 91 IRON (HEME PROXIMAL LIGAND).
 FT TURN 4 5
 FT HELIX 6 13
 FT TURN 14 16
 FT TURN 20 21
 FT TURN 22 30
 FT TURN 31 33
 FT TURN 35 36
 FT TURN 38 40
 FT TURN 41 43
 FT HELIX 50 55
 FT TURN 57 57
 FT TURN 58 65
 FT TURN 66 66
 FT TURN 68 72
 FT TURN 85 86
 FT TURN 87 93
 FT TURN 94 95
 FT HELIX 99 117
 FT TURN 119 120
 FT HELIX 123 142
 SQ SEQUENCE 145 AA; 15824 MW; F3875A54C4C84323 CRC64;
 Query Match 100.0%; Score 58; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 0.0049;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPWTQRF 10
 Db 31 LVVYPWTQRF 40
 RESULT 15
 HBB_OVIMU STANDARD; PRT; 145 AA.
 ID HBB_OVIMU
 AC P02076;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.

GN HBB.
OS Ovis orientalis musimon (Mouflon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9938;
RN [1]
RP SEQUENCE OF 1-103 AND 116-145.
RX MEDLINE=71089262; PubMed=5496230;
RA Wilson J.B., Miller A., Huismann T.H.J.;
RT "production of hemoglobin C in the Mouflon (Ovis musimon Pallas,
RT 1811) and the Barbary sheep (Ammotragus lervia Pallas, 1777) during
RT experimental anemia: amino acid composition of tryptic peptides from
RT the beta B and bet C chains.";
RL Biochem. Genet. 4:677-688(1970).
CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -!- MISCELLANEOUS: THIS BETA CHAIN IS TERMED THE B ALLELE, EVEN THOUGH
CC IT MORE CLOSELY RESEMBLES THE SHEEP A ALLELE.
CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR: S16377; S16377.
DR HSP: P02070; 1FSX.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 62 62 IRON (HEME DISTAL LIGAND).
FT METAL 91 91 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 145 AA; 16108 MW; 50C7CDBB8AD3F5DD CRC64;

Query Match 100.0%; Score 58; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 31 LVVYPWTQRF 40
|||||

Search completed: February 24, 2003, 11:01:40
Job time : 10 secs